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ning of each regular issue of the PCT Gazette.

(54) Title: PATHOGEN TOLERANCE GENES

(57) Abstract: The present invention relates to transgenic plants and methods of making transgenic plant using punitive transcription factors that modulate the transgenic plant's susceptibility to disease.



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PATHOGEN TOLERANCE GENES

RELATED APPLICATION INFORMATION

The present invention claims the benefit from US Provisional Patent Application
5 Serial Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and
"Plant Trait Modification III" filed August 22, 2000.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the
present invention pertains to compositions and methods for phenotypically modifying a plant.

BACKGROUND OF THE INVENTION

10 Transcription factors can modulate gene expression, either increasing or
decreasing (inducing or repressing) the rate of transcription. This modulation results in
differential levels of gene expression at various developmental stages, in different tissues and
cell types, and in response to different exogenous (e.g., environmental) and endogenous
15 stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological
pathways, altering the expression levels of one or more transcription factors can change entire
biological pathways in an organism. For example, manipulation of the levels of selected
transcription factors may result in increased expression of economically useful proteins or
20 metabolic chemicals in plants or to improve other agriculturally relevant characteristics.
Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis
of unwanted compounds or remove an undesirable trait. Therefore, manipulating
transcription factor levels in a plant offers tremendous potential in agricultural biotechnology
for modifying a plant's traits.

25 The present invention provides novel transcription factors useful for
modifying a plant's phenotype in desirable ways, such as modifying a plant's pathogen
tolerance.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide
30 comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide
sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N,
where N=1-29, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence
encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of
(a); (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-
35 1, where N=1-29, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence

comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a
5 nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's pathogen tolerance; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which
10 encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where
15 N=1-29. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the
20 recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention may
25 be a plant lacking a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29.

The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce,
30 mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

35 In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having improved pathogen tolerance. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified pathogen tolerance.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant pathogen tolerance phenotype.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant pathogen tolerance phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's pathogen tolerance when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying traits associated with a plant's pathogen tolerance, such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, alterations in the cell death response, or the like. Transgenic plants employing the polynucleotides or polypeptides of the invention are more tolerant to biotrophic or necrotrophic pathogens such as fungi, bacteria, mollicutes, viruses, nematodes, parasitic higher plants or the like.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol.

Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. 9: 597-604);
 5 the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

15 In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially
 20 complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, of as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

25 A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide
 30 may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA,
 35 a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant

tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2%

increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenolipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's pathogen tolerance.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence

analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

5 Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according
10 to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention were ectopically expressed in
15 overexpressor or knockout plants and changes in the pathogen tolerance of the plants was observed. Therefore, the polynucleotides and polypeptides can be employed to improve the pathogen resistance of plants.

Making polynucleotides

The polynucleotides of the invention include sequences that encode
20 transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both
25 sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such
30 as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the
35 art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger");

Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented
5 through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the
10 ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids
15 are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase
20 and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part
25 of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can
30 be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be
35 derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn,

potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 31% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under
5 defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For identification of less
10 closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to
15 the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes
20 to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

25 Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies
30 (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression
35 library produced from the plant from which it is desired to clone additional transcription

factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acids			Codon						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	TGC	TGT					
Aspartic acid	Asp	D	GAC	GAT					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	TTC	TTT					
Glycine	Gly	G	GGA	GGC	GGG	GGT			
Histidine	His	H	CAC	CAT					
Isoleucine	Ile	I	ATA	ATC	ATT				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT	
Methionine	Met	M	ATG						
Asparagine	Asn	N	AAC	AAT					
Proline	Pro	P	CCA	CCC	CCG	CCT			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT	
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT	
Threonine	Thr	T	ACA	ACC	ACG	ACT			
Valine	Val	V	GTA	GTC	GTG	GTT			
Tryptophan	Trp	W	TGG						
Tyrosine	Tyr	Y	TAC	TAT					

15

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

20

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

25

30

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Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) *Nature* 370:389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of

the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51: 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant

Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

5 Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-
10 Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

15 Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a
20 transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

 Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (see, e.g., Odel et al. (1985) Nature
25 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

 A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on
30 the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For
35 example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the

2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences.

These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation

codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with
5 vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral
10 particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook
15 and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation
20 (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO
25 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

30 The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

35 For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the

expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After

identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified
5 by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that
10 modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

15 The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator
20 protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription
25 of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for
30 compounds that interfere with the TF protein-protein interactions can be preformed.

IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate
35 molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the

expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of
5 microarrays, Northern, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

10 Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which
15 the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a
20 combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

25 A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set
30 length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993);
35 isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating
5 chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and
10 robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available.
15 These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

20 The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to
25 identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with
30 cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids
35 and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A

subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

5 The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the pathogen resistance of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared
10 with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved pathogen tolerance, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

15 In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof,
20 can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple
25 oligonucleotide sequences and catalytic sequences such as ribozymes.

 For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or
30 homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of
35 shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various

lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single

transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Patent No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco,

peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

5 Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are
10 not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the
15 sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526;
20 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the
25 antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by
30 analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of
35 one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may

be used to associate or link certain functional benefits, such improved pathogen tolerance, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin
5 Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local
10 homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed
15 by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

20 A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of
25 skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information
30 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for
35 initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters

M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may be implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or

wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

20 EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to
5 generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE
10 fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers
15 specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours.
20 The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16
25 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini
30 Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF AGROBACTERIUM WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of
35 *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml

LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled
5 buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described
10 above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After
15 electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR
20 amplification and sequence analysis.

EXAMPLE IV. TRANSFORMATION OF ARABIDOPSIS PLANTS WITH AGROBACTERIUM TUMEFACIENS WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to
25 transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM
30 benzylamino purine (Sigma), 200 µl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under
35 continuous illumination (50-75 µE/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of

multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T₁ generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T₂) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 bases to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

15 EXAMPLE VII. IDENTIFICATION OF PATHOGEN INDUCED GENES

In some instances, expression patterns of the pathogen induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagegene a software purchased from BioDiscovery (Los Angeles, CA).

EXAMPLE VIII. IDENTIFICATION OF PATHOGEN TOLERANCE PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotrophic fungal pathogens, such as *Erysiphe orontii*; and necrotrophic fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

Botrytis cinerea is a necrotrophic pathogen. *Botrytis cinerea* was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (-sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens *Pseudomonas syringae* pv *maculicola* strain 4326 and pv *maculicola* strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

Table 3

SEQ ID No.	GID	Knockout (KO) or overexpressor (OE)	Phenotype
1	G188	KO	Increased susceptibility to Fusarium
3	G616	OE	Increased tolerance to Erysiphe
5	G19	OE	Increased tolerance to Erysiphe
7	G261	OE	Increased susceptibility to Botrytis
9	G28	OE	Increased resistance to Erysiphe
11	G869	OE	Increased susceptibility to Fusarium
13	G237	OE	Increased tolerance to Erysiphe
15	G409	OE	Increased tolerance to Erysiphe
17	G418	OE	Increased tolerance to Pseudomonas
19	G591	OE	Increased tolerance to Erysiphe
21	G525	OE	Increased tolerance to Pseudomonas
23	G545	OE	Increased susceptibility to Pseudomonas, Erysiphe and Fusarium
25	G865	OE	Increased susceptibility to Erysiphe and Botrytis
27	G881	OE	Increased susceptibility to Erysiphe and Botrytis
29	G896	KO	Increased susceptibility to Fusarium
31	G378	OE	Increased resistance to Erysiphe
33	G569	OE	Decreased expression of defense genes
35	G558	OE	Increased expression of defense genes

5 For a particular overexpressor that shows an increased susceptibility to a pathogen, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows an increased susceptibility to a pathogen, it may be more useful to select a plant with an increased expression of the particular transcription factor.

10 Other than *Fusarium oxysporum*, *Erysiphe orontii*, the transgenic plants are more tolerant to *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp.*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp.*, *Fusarium solani*, or the like. The transgenic plants are more resistant to fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf
15 blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial wilt, soft rot of vegetables, and the like; nematode diseases such as root knot, sugar beet cyst nematode or the like.

20

EXAMPLE IX. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-58 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs Nos. 1-58, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of $3.6e-40$ is 3.6×10^{-40} . For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-*Arabidopsis* genes shown in Figure 3 and the *Arabidopsis* genes in the sequence listing are: SEQ ID No. 1: 38%-76%; SEQ ID No. 3: 36%-72%; SEQ ID No. 5: 51%-75%; SEQ ID No. 7: 37%-76%; SEQ ID No. 9: 48%-75%; SEQ ID No. 11: 31%-68%; SEQ ID No. 13: 59%-81%; SEQ ID No. 15: 49%-81%; SEQ ID No. 17: 53%-87%; SEQ ID No. 19: 48%-84%; SEQ ID No. 21: 73%-89%; SEQ ID No. 23: 52%-64%; SEQ ID No. 25: 48%-83%; SEQ ID No. 27: 35%-92%; SEQ ID No. 29: 56%-89%; SEQ ID No. 31: 50%-90%; SEQ ID No. 33: 50%-93%; SEQ ID No. 35: 52%-81%; SEQ ID No. 37: 75%-81%; SEQ ID No. 39: 35%-72%; SEQ ID No. 41: 55%-89%; SEQ ID No. 43: 56%-77%; SEQ ID No. 45: 34%-72%; SEQ ID No. 47: 51%-86%; SEQ ID No. 49: 46%-86%; SEQ ID No. 51: 58%-80%; SEQ ID No. 53: 46%-55%; SEQ ID No. 55: 84%-89%; and SEQ ID No. 57: 43%-71%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the pathogen tolerance of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A transgenic plant with modified pathogen tolerance, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - 5 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29, or a complementary nucleotide sequence thereof;
 - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
 - 10 (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-29, or a complementary nucleotide sequence thereof;
 - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
 - (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide
 - 15 sequence of one or more of: (a), (b), (c), or (d);
 - (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
 - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's
 - 20 pathogen tolerance;
 - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
 - (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
 - 25 (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29;
 - (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and
 - (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence
 - 30 identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-29.
2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.
- 35 3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot,

cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

- 5 4. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- 10 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29, or a complementary nucleotide sequence thereof;
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-29, or a complementary nucleotide sequence thereof;
- 15 (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
- 20 (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's pathogen tolerance;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- 25 (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and
- 30 (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-29.
- 35 5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.

6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.
7. A cell comprising the cloning or expression vector of claim 6.
8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.
9. A composition produced by one or more of:
- (a) incubating one or more polynucleotide of claim 4 with a nuclease;
 - (b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;
 - (c) incubating one or more polynucleotide of claim 4 with a polymerase;
 - (d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;
 - (e) incubating one or more polynucleotide of claim 4 with a cloning vector, or
 - (f) incubating one or more polynucleotide of claim 4 with a cell.
10. A composition comprising two or more different polynucleotides of claim 4.
11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.
12. A plant comprising an isolated polypeptide of claim 11.
13. A method for producing a plant having a modified pathogen tolerance, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for improved pathogen tolerance thereby providing the modified plant with a modified pathogen tolerance.
14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.
15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:
- (a) expressing a polypeptide encoded by the polynucleotide in a plant; and
 - (b) identifying at least one factor that is modulated by or interacts with the polypeptide.

16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.
- 5 17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.
18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:
- 10 (a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,
- (b) monitoring one or more of:
- (i) expression level of the polynucleotide in the plant;
- (ii) expression level of the polypeptide in the plant;
- 15 (iii) modulation of an activity of the polypeptide in the plant; or
- (iv) modulation of an activity of the polynucleotide in the plant.
19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide
- 20 encoded by the polynucleotide.
20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant pathogen tolerance phenotype.
- 25 21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:
- (a) providing a sequence database; and,
- 30 (b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.
- 35 22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.
- 5
24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant pathogen tolerance phenotype.
- 10
25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.
26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.
- 15
27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G188	cDNA	
2	G188	protein	175-222
3	G616	cDNA	
4	G616	protein	39-95
5	G19	cDNA	
6	G19	protein	76-145
7	G261	cDNA	
8	G261	protein	16-104
9	G28	cDNA	
10	G28	protein	145-213
11	G869	cDNA	
12	G869	protein	109-177
13	G237	cDNA	
14	G237	protein	11-113
15	G409	cDNA	
16	G409	protein	64-124
17	G418	cDNA	
18	G418	protein	500-560
19	G591	cDNA	
20	G591	protein	143-240
21	G525	cDNA	
22	G525	protein	23-167
23	G545	cDNA	
24	G545	protein	82-102, 136-154
25	G865	cDNA	
26	G865	protein	36-103
27	G881	cDNA	
28	G881	protein	176-233
29	G896	cDNA	
30	G896	protein	18-39
31	G378	cDNA	
32	G378	protein	196-237
33	G569	cDNA	
34	G569	protein	90-153
35	G558	cDNA	
36	G558	protein	45-105

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
37	G1396	homolog of G1394	cDNA	
38	G1396	homolog of G1394	protein	entire protein
39	G265	homolog of G261	cDNA	
40	G265	homolog of G261	protein	14-105
41	G1006	homolog of G28	cDNA	
42	G1006	homolog of G28	protein	114-182
43	G1309	homolog of G237	cDNA	
44	G1309	homolog of G237	protein	9-114
45	G2550	homolog of G418	cDNA	
46	G2550	homolog of G418	protein	348-408
47	G965	homolog of G418	cDNA	
48	G965	homolog of G418	protein	423-486
49	G793	homolog of G591	cDNA	
50	G793	homolog of G591	protein	151-206
51	G764	homolog of G525	cDNA	
52	G764	homolog of G525	protein	27-171
53	G350	homolog of G545	cDNA	
54	G350	homolog of G545	protein	91-113,150-170
55	G986	homolog of G881	cDNA	
56	G986	homolog of G881	protein	146-203
57	G1349	homolog of G896	cDNA	
58	G1349	homolog of G896	protein	13-63

Figure 3A

SEQ ID No.	GID	Genbank NID	P-value	Species
1	G188	7779802	5.20E-36	Lotus japonicus
1	G188	7284340	2.10E-34	Glycine max
1	G188	9361307	1.20E-27	Triticum aestivum
1	G188	7340336	1.10E-22	Oryza sativa
1	G188	6529152	3.60E-22	Lycopersicon esculentum
1	G188	8748477	7.70E-21	Medicago truncatula
1	G188	5456433	7.10E-14	Zea mays
1	G188	9302479	1.60E-12	Sorghum bicolor
1	G188	6696287	4.10E-12	Pinus taeda
1	G188	562242	9.00E-12	Brassica rapa
3	G616	7719440	8.30E-37	Lotus japonicus
3	G616	7692230	5.90E-33	Glycine max
3	G616	7501307	1.10E-21	Gossypium arboreum
3	G616	8071090	1.50E-21	Solanum tuberosum
3	G616	8858771	1.50E-21	Oryza sativa
3	G616	5047315	1.50E-21	Gossypium hirsutum
3	G616	6358532	5.80E-20	Antirrhinum graniticum
3	G616	2826867	7.00E-20	Antirrhinum majus
3	G616	6358535	7.40E-20	Antirrhinum majus subsp. linkianum
3	G616	6358538	7.50E-20	Antirrhinum braun-blanquetii
5	G19	8789223	2.80E-34	Citrus x paradisi
5	G19	9434234	4.50E-34	Lycopersicon esculentum
5	G19	7478682	1.30E-30	Glycine max
5	G19	6654934	1.20E-28	Medicago truncatula
5	G19	3264766	5.50E-26	Prunus armeniaca
5	G19	7624302	8.30E-26	Gossypium arboreum
5	G19	9425363	2.90E-25	Triticum aestivum
5	G19	688579	3.60E-25	Ricinus communis
5	G19	9419304	6.00E-25	Hordeum vulgare
5	G19	7720316	8.80E-25	Lotus japonicus
7	G261	5821137	5.10E-93	Nicotiana tabacum
7	G261	7158881	8.80E-86	Medicago sativa
7	G261	886741	1.00E-73	Zea mays
7	G261	5900449	5.20E-47	Lycopersicon esculentum
7	G261	7561318	1.20E-46	Medicago truncatula
7	G261	19491	1.70E-42	Lycopersicon peruvianum
7	G261	7233914	3.50E-41	Glycine max
7	G261	4528238	9.00E-41	Citrus unshiu
7	G261	8903922	4.00E-39	Hordeum vulgare
7	G261	9251913	1.90E-36	Solanum tuberosum
9	G28	7528275	4.20E-62	Mesembryanthemum crystallinum
9	G28	6654776	1.20E-57	Medicago truncatula
9	G28	790362	2.30E-54	Nicotiana tabacum
9	G28	8809570	8.00E-54	Nicotiana glauca
9	G28	3342210	8.40E-54	Lycopersicon esculentum
9	G28	6566281	8.40E-47	Glycine max
9	G28	7627061	8.40E-47	Gossypium arboreum
9	G28	7324479	2.00E-44	Lycopersicon pennellii
9	G28	6478844	1.80E-35	Matricaria chamomilla
9	G28	7273972	7.80E-29	Oryza sativa
11	G869	2213784	1.30E-19	Lycopersicon esculentum
11	G869	3065894	7.30E-19	Nicotiana tabacum

Figure 3B

SEQ ID No.	GID	Genbank NID	P-value	Species
11	G869	8570080	4.20E-18	Oryza sativa
11	G869	7560260	1.50E-17	Medicago truncatula
11	G869	7534890	5.20E-14	Sorghum bicolor
11	G869	6455322	1.10E-13	Glycine max
11	G869	9362061	2.70E-13	Triticum aestivum
11	G869	7788764	5.70E-13	Lotus japonicus
11	G869	7624302	2.50E-12	Gossypium arboreum
11	G869	3858036	2.80E-12	Populus balsamifera subsp. trichocarpa
13	G237	8283916	4.70E-42	Glycine max
13	G237	9361969	8.30E-41	Triticum aestivum
13	G237	4753385	4.10E-39	Zea mays
13	G237	7535969	4.10E-33	Sorghum bicolor
13	G237	7566043	9.30E-33	Medicago truncatula
13	G237	7339127	2.00E-32	Lycopersicon esculentum
13	G237	5860031	1.10E-28	Pinus taeda
13	G237	7776223	2.20E-28	Lotus japonicus
13	G237	6850206	5.10E-28	Oryza sativa
13	G237	5048991	8.50E-28	Gossypium hirsutum
15	G409	6654773	6.10E-57	Medicago truncatula
15	G409	6531235	2.00E-56	Lycopersicon esculentum
15	G409	7924152	1.10E-47	Glycine max
15	G409	5006854	6.50E-43	Oryza sativa
15	G409	8098529	2.10E-41	Hordeum vulgare
15	G409	767697	1.40E-37	Daucus carota
15	G409	8328991	3.30E-37	Mesembryanthemum crystallinum
15	G409	7415613	1.40E-32	Physcomitrella patens
15	G409	7785121	2.80E-32	Lotus japonicus
15	G409	6916941	4.80E-32	Lycopersicon pennellii
17	G418	7239156	1.90E-123	Malus x domestica
17	G418	5892190	2.00E-62	Lycopersicon esculentum
17	G418	7628137	8.70E-58	Gossypium arboreum
17	G418	9205496	3.90E-51	Glycine max
17	G418	6069643	1.50E-45	Oryza sativa
17	G418	7562931	6.90E-45	Medicago truncatula
17	G418	7781695	5.50E-40	Lotus japonicus
17	G418	9298824	7.80E-34	Sorghum bicolor
17	G418	9428023	3.90E-32	Triticum aestivum
17	G418	7244366	1.30E-31	Mentha x piperita
19	G591	7646333	1.90E-55	Lycopersicon esculentum
19	G591	7924288	4.10E-53	Glycine max
19	G591	7722838	1.10E-41	Lotus japonicus
19	G591	5804781	1.40E-24	Nicotiana tabacum
19	G591	9198126	2.50E-23	Medicago truncatula
19	G591	427677	9.50E-15	Oryza sativa
19	G591	7624745	1.80E-14	Gossypium arboreum
19	G591	7535578	8.70E-14	Sorghum bicolor
19	G591	5915205	1.30E-11	Zea mays
19	G591	9249806	2.60E-11	Solanum tuberosum
21	G525	4384535	5.60E-61	Lycopersicon esculentum
21	G525	6454868	2.00E-58	Glycine max
21	G525	6066594	9.30E-54	Petunia x hybrida
21	G525	4977542	8.60E-51	Oryza sativa

Figure 3C

SEQ ID No.	GID	Genbank NID	P-value	Species
21	G525	9361647	2.50E-50	Triticum aestivum
21	G525	4218536	5.20E-50	Triticum sp.
21	G525	6732159	5.20E-50	Triticum monococcum
21	G525	5343151	2.70E-49	Zea mays
21	G525	5049217	4.20E-48	Gossypium hirsutum
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23	G545	4666359	8.30E-55	Datisca glomerata
23	G545	7228328	3.70E-52	Medicago sativa
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23	G545	7206360	3.10E-44	Medicago truncatula
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23	G545	439492	3.90E-39	Petunia x hybrida
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23	G545	7322653	6.80E-37	Lycopersicon hirsutum
23	G545	7785845	1.10E-33	Lotus japonicus
25	G865	9417297	1.70E-32	Triticum aestivum
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25	G865	7528275	5.90E-21	Mesembryanthemum crystallinum
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27	G881	5820418	9.80E-29	Glycine max
27	G881	8440065	1.00E-27	Gossypium hirsutum
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27	G881	8205146	5.20E-21	Oryza sativa
27	G881	1159878	8.20E-17	Avena fatua
27	G881	9299778	2.70E-16	Sorghum bicolor
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29	G896	7628908	3.60E-82	Gossypium arboreum
29	G896	7244408	1.80E-79	Mentha x piperita
29	G896	5046180	2.10E-73	Gossypium hirsutum
29	G896	7678652	1.10E-63	Lotus japonicus
29	G896	8286031	1.40E-60	Glycine max
29	G896	5888938	4.50E-58	Lycopersicon esculentum
29	G896	9298238	9.20E-54	Sorghum bicolor
29	G896	7566414	8.00E-52	Medicago truncatula
29	G896	8845076	1.00E-46	Triticum aestivum
31	G378	5270028	5.10E-73	Lycopersicon esculentum
31	G378	5048335	4.10E-58	Gossypium hirsutum
31	G378	7239521	5.90E-42	Oryza sativa
31	G378	5606120	6.80E-36	Glycine max
31	G378	3853800	3.20E-30	Populus tremula x Populus tremuloides
31	G378	7659983	1.70E-23	Sorghum bicolor

Figure 3D

SEQ ID No.	GID	Genbank NID	P-value	Species
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31	G378	3242033	4.30E-17	Mesembryanthemum crystallinum
31	G378	7626259	7.70E-13	Gossypium arboreum
33	G229	7337390	6.60E-51	Lycopersicon esculentum
33	G229	9823237	3.60E-50	Hordeum vulgare
33	G229	7244424	4.90E-50	Mentha x piperita
33	G229	7776053	1.70E-49	Lotus japonicus
33	G229	2921335	5.80E-48	Gossypium hirsutum
33	G229	1491932	4.50E-47	Zea mays
33	G229	6455590	2.80E-44	Glycine max
33	G229	6020191	2.00E-41	Pinus taeda
33	G229	10697236	4.20E-41	Oryza sativa
33	G229	7765706	5.10E-41	Medicago truncatula
35	G663	7673087	5.10E-43	Petunia integrifolia
35	G663	9508051	3.00E-41	Lycopersicon esculentum
35	G663	7673091	3.30E-41	Petunia x hybrida
35	G663	7673097	2.40E-36	Petunia axillaris
35	G663	5048991	1.20E-33	Gossypium hirsutum
35	G663	6455590	2.50E-31	Glycine max
35	G663	7560175	1.90E-27	Medicago truncatula
35	G663	7244424	4.10E-26	Mentha x piperita
35	G663	9954117	3.40E-25	Solanum tuberosum
35	G663	6020191	3.60E-25	Pinus taeda
37	G1396	498704	5.20E-22	Spinacia oleracea
37	G1396	7502400	1.20E-21	Gossypium arboreum
37	G1396	3857536	3.40E-21	Populus balsamifera subsp. trichocarpa
37	G1396	4385300	1.20E-20	Lycopersicon esculentum
37	G1396	6917249	1.50E-20	Lycopersicon pennellii
37	G1396	6915979	1.70E-20	Glycine max
37	G1396	7674530	2.70E-20	Medicago truncatula
37	G1396	8090319	3.40E-20	Sorghum bicolor
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37	G1396	6654124	1.10E-19	Zea mays
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39	G265	7158881	3.80E-79	Medicago sativa
39	G265	886741	1.60E-70	Zea mays
39	G265	5900449	5.60E-43	Lycopersicon esculentum
39	G265	8903922	8.20E-43	Hordeum vulgare
39	G265	7561318	2.10E-41	Medicago truncatula
39	G265	9204445	5.30E-36	Glycine max
39	G265	4528238	5.40E-36	Citrus unshiu
39	G265	19489	2.10E-35	Lycopersicon peruvianum
39	G265	9251913	2.00E-32	Solanum tuberosum
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41	G1006	3342210	4.90E-49	Lycopersicon esculentum
41	G1006	6654776	1.90E-48	Medicago truncatula
41	G1006	790362	2.30E-47	Nicotiana tabacum
41	G1006	8809570	2.00E-46	Nicotiana glauca
41	G1006	7627061	6.40E-41	Gossypium arboreum
41	G1006	7324479	1.20E-35	Lycopersicon pennellii
41	G1006	6478844	1.80E-35	Matricaria chamomilla

Figure 3E

SEQ ID No.	GID	Genbank NID	P-value	Species
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43	G1309	7566043	9.60E-35	Medicago truncatula
43	G1309	5891104	2.20E-31	Lycopersicon esculentum
43	G1309	5860031	2.10E-30	Pinus taeda
43	G1309	5049507	6.20E-30	Gossypium hirsutum
43	G1309	5139805	1.30E-29	Glycine max
43	G1309	6850206	2.50E-29	Oryza sativa
43	G1309	7721017	3.40E-29	Lotus japonicus
43	G1309	8368245	5.20E-28	Zea mays
43	G1309	20560	9.50E-27	Petunia x hybrida
45	G2550	4380729	2.80E-51	Lycopersicon esculentum
45	G2550	5667196	2.20E-49	Oryza sativa
45	G2550	8669454	1.40E-48	Glycine max
45	G2550	9298824	1.50E-48	Sorghum bicolor
45	G2550	7239156	9.90E-46	Malus x domestica
45	G2550	7570704	5.70E-45	Medicago truncatula
45	G2550	7628137	3.30E-42	Gossypium arboreum
45	G2550	7244366	6.00E-41	Mentha x piperita
45	G2550	9428023	4.70E-40	Triticum aestivum
45	G2550	9250642	3.50E-39	Solanum tuberosum
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47	G965	5892190	2.00E-62	Lycopersicon esculentum
47	G965	7628137	1.60E-56	Gossypium arboreum
47	G965	9205496	2.60E-49	Glycine max
47	G965	6069643	1.70E-45	Oryza sativa
47	G965	7562931	2.50E-44	Medicago truncatula
47	G965	7781695	1.60E-41	Lotus japonicus
47	G965	9298824	6.30E-33	Sorghum bicolor
47	G965	9428023	1.50E-31	Triticum aestivum
47	G965	7244366	1.20E-29	Mentha x piperita
49	G793	6976712	3.60E-43	Lycopersicon esculentum
49	G793	7924288	2.00E-41	Glycine max
49	G793	7614163	3.90E-34	Lotus japonicus
49	G793	9198126	5.70E-23	Medicago truncatula
49	G793	5804781	1.10E-22	Nicotiana tabacum
49	G793	7535578	1.60E-14	Sorghum bicolor
49	G793	427677	6.10E-14	Oryza sativa
49	G793	5915205	2.90E-10	Zea mays
49	G793	9249806	4.20E-10	Solanum tuberosum
49	G793	7624745	1.30E-09	Gossypium arboreum
51	G764	4384535	7.00E-70	Lycopersicon esculentum
51	G764	5049217	1.80E-65	Gossypium hirsutum
51	G764	6454868	1.90E-64	Glycine max
51	G764	6066594	5.20E-59	Petunia x hybrida
51	G764	4218536	2.30E-52	Triticum sp.
51	G764	6732159	2.30E-52	Triticum monococcum
51	G764	9361647	7.50E-52	Triticum aestivum
51	G764	4977542	4.10E-49	Oryza sativa
51	G764	6799764	4.40E-49	Medicago truncatula
51	G764	9296257	1.00E-48	Sorghum bicolor

Figure 3F

SEQ ID No.	GID	Genbank NID	P-value	Species
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53	G350	4666359	3.10E-48	Datisca glomerata
53	G350	1763062	8.30E-48	Glycine max
53	G350	7626808	9.10E-44	Gossypium arboreum
53	G350	7206360	2.20E-43	Medicago truncatula
53	G350	2981168	2.10E-38	Nicotiana tabacum
53	G350	7322653	2.00E-37	Lycopersicon hirsutum
53	G350	5276755	2.40E-37	Lycopersicon esculentum
53	G350	2058503	1.10E-31	Brassica rapa
55	G986	6472584	1.00E-34	Nicotiana tabacum
55	G986	8440065	8.80E-33	Gossypium hirsutum
55	G986	4385167	1.50E-32	Lycopersicon esculentum
55	G986	8205146	5.50E-30	Oryza sativa
55	G986	5820418	8.80E-26	Glycine max
55	G986	1159878	2.30E-23	Avena fatua
55	G986	9250698	4.60E-22	Solanum tuberosum
55	G986	9413507	7.90E-21	Triticum aestivum
55	G986	7748539	2.30E-20	Lotus japonicus
55	G986	9199620	1.30E-16	Medicago truncatula
57	G1349	8904043	1.50E-47	Hordeum vulgare
57	G1349	7244408	2.40E-47	Mentha x piperita
57	G1349	8286031	3.60E-46	Glycine max
57	G1349	9298238	9.10E-36	Sorghum bicolor
57	G1349	7628908	4.70E-34	Gossypium arboreum
57	G1349	5046180	1.50E-33	Gossypium hirsutum
57	G1349	5888938	1.30E-30	Lycopersicon esculentum
57	G1349	5043924	6.20E-30	Pinus taeda
57	G1349	8845076	4.40E-29	Triticum aestivum
57	G1349	7678652	4.20E-27	Lotus japonicus

MBI15 Sequence Listing.ST25
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Ratcliffe, Oliver
Creelman, Robert
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cat cag tca ttc ctc gct aat cta cag agg ttt cca aca tca gaa agt      1082
His Gln Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser
                305                      310                      315

gga gga ggt cca cag ttc tta ttc ggt gca ctg cct gca gag aat cac      1130
Gly Gly Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His
                320                      325                      330

cac cac aat cac cag ttt cag ctt tac tat gaa aat gga tgc aga aac      1178
His His Asn His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn
335                      340                      345                      350

tca tca gaa cat aag ggt aaa ggc aag aac tga tgatattaat tattgcatct      1231
Ser Ser Glu His Lys Gly Lys Gly Lys Asn
                355                      360

ttggttttgt tcaaatgctc attttgtatg tttatctttg gtttatttca aaacaaatgt      1291

taatctcttt cgttgtctga tgtgtgttag ggttttgttt tatgtattga gggctcttgg      1351

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 <212> PRT
 <213> Arabidopsis thaliana

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20 25 30

Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys
35 40 45

Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln
50 55 60

Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala
65 70 75 80

MBI15 Sequence Listing.ST25

Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Ser Glu Leu Pro
 85 90 95
 Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His Gln Asn
 100 105 110
 Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys
 115 120 125
 Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Ser Gly Leu Ser Leu Ser
 130 135 140
 Arg Ser Glu Leu Arg Asp Lys Ala Arg Glu Arg Ala Arg Glu Arg Thr
 145 150 155 160
 Ala Lys Glu Thr Lys Glu Arg Asp His Asn His Thr Ser Phe Thr Asp
 165 170 175
 Leu Leu Asn Ser Gly Ser Asp Pro Val Asn Ser Asn Arg Gln Trp Met
 180 185 190
 Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly Leu
 195 200 205
 Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn Ser
 210 215 220
 His Pro Phe Ser Ser Ile Ser Asp His His His His His Pro His His
 225 230 235 240
 Gln His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala
 245 250 255
 Glu Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro
 260 265 270
 Ser Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser
 275 280 285
 Gly Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln
 290 295 300
 Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly
 305 310 315 320
 Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His
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 Glu His Lys Gly Lys Gly Lys Asn
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Met Cys Gly Gly Ala Ile Ile Ser Asp Tyr Ala Pro Leu Val																	
1 5 10																	
acc aag gcc aag ggc cgt aaa ctc acg gct gag gaa ctc tgg tca gag																	159
Thr Lys Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu																	
15 20 25 30																	
ctc gat gct tcc gcc gcc gac gac ttc tgg ggt ttc tat tcc acc tcc																	207
Leu Asp Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser																	
35 40 45																	
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Lys Leu His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys																	
50 55 60																	
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Lys Glu Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val																	
65 70 75																	
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Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile																	
80 85 90																	
cga gat cca cga aaa ggt gtt aga gtt tgg ctt ggt acg ttc aac acg																	399
Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr																	
95 100 105 110																	
gcg gag gaa gct gcc atg gct tat gat gtt gcg gcc aag cag atc cgt																	447
Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg																	
115 120 125																	
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Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro																	
130 135 140																	
cct aat tat act cct ccg ccg tca tcg cca cga tca acc gat cag cct																	543
Pro Asn Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro																	
145 150 155																	
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Pro Ala Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser																	
160 165 170																	
cag ccg agt ttc ccg gtg gag tgt ata gga ttt gga aat ggg gac gag																	639
Gln Pro Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu																	
175 180 185 190																	
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Phe Gln Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln																	
195 200 205																	
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Gln Ile Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala																	
210 215 220																	
gag caa ccg agt cag ctt gat gag tcc gtt tcc gag gtg gat atg tgg																	783
Glu Gln Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp																	
225 230 235																	
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Met Leu Asp Asp Val Ile Ala Ser Tyr Glu																	

MBI15 Sequence Listing.ST25

240
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 aaaaagttaa ataaagtctg taatatatat gtaaccgccg ttacttttta aaggttttta 896
 ccgtcgcatt ggactgctga tgatgtctgt tgtgtaatgt gtagaatgtg accaaatgga 956
 cgttatatta cggtttgtgg tattattagt ttcttagatg gaaaaactta catgtgtaaa 1016
 taagatttgt aatgtaagac gaagtactta taacttctt 1055

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 Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu
 35 40 45
 His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu
 50 55 60
 Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg
 65 70 75 80
 Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 85 90 95
 Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
 100 105 110
 Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp
 115 120 125
 Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn
 130 135 140
 Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala
 145 150 155 160
 Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro
 165 170 175
 Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln
 180 185 190
 Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile
 195 200 205
 Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln
 210 215 220
 Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp Met Leu

MBI15 Sequence Listing.ST25

225

230

235

240

Asp Asp Val Ile Ala Ser Tyr Glu
245

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<223> G261

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gcttttgctt gattgtcttt tatttagaaa cagtgggtgag, ttttttagtct ttcactttgt 180
tcaagttcga agcttttttt ggaggggaatt ttgggcttct gattttgatc gaaacttact 240
gatagtaagt tctttgagtc ctctttaact gtagtttctg tgtactgaag ttattgaatt 300
gaaagttttt atcttttttg gttattgaaa ctttcatagt ttgatcaaaa gagtctcttg 360
ctctgttttt ggctctgttt ttgtgagtgt gattgtaagc tttgttgtga gtagattgaa 420
tcaaggagtg tgagagttgt taaaagtgtt ttcagag atg gat gag aat aat cat 475
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1 5
gga gtt tca tca agc tca ctt cca cct ttc ctc acc aaa aca tat gag 523
Gly Val Ser Ser Ser Ser Leu Pro Pro Phe Leu Thr Lys Thr Tyr Glu
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Met Val Asp Asp Ser Ser Ser Asp Ser Ile Val Ser Trp Ser Gln Ser
25 30 35
aat aag agt ttc atc gtt tgg aat ccg ccg gag ttt tct aga gat ctt 619
Asn Lys Ser Phe Ile Val Trp Asn Pro Pro Glu Phe Ser Arg Asp Leu
40 45 50
ctt ccg aga ttc ttc aag cac aat aac ttc tct agc ttt atc cgc cag 667
Leu Pro Arg Phe Phe Lys His Asn Asn Phe Ser Ser Phe Ile Arg Gln
55 60 65 70
ctt aac aca tat ggt ttt aga aaa gct gat cct gag caa tgg gaa ttt 715
Leu Asn Thr Tyr Gly Phe Arg Lys Ala Asp Pro Glu Gln Trp Glu Phe
75 80 85
gcg aat gat gat ttt gtg aga ggt caa cct cat ctt atg aag aac att 763
Ala Asn Asp Asp Phe Val Arg Gly Gln Pro His Leu Met Lys Asn Ile
90 95 100
cat aga cgc aaa cca gtt cat agc cac tct tta ccg aat ctt caa gct 811
His Arg Arg Lys Pro Val His Ser His Ser Leu Pro Asn Leu Gln Ala
105 110 115
cag tta aac ccg ttg acg gat tca gaa cga gtg aga atg aat aat cag 859
Gln Leu Asn Pro Leu Thr Asp Ser Glu Arg Val Arg Met Asn Asn Gln
120 125 130
att gag aga ttg aca aaa gag aaa gaa gga ttg ctt gaa gag tta cat 907
Ile Glu Arg Leu Thr Lys Glu Lys Glu Gly Leu Leu Glu Glu Leu His
135 140 145 150
aaa caa gac gag gaa cga gaa gtg ttt gag atg caa gtg aaa gaa ctt 955
Lys Gln Asp Glu Glu Arg Glu Val Phe Glu Met Gln Val Lys Glu Leu

MBI15 Sequence Listing.ST25

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ccg tgt gtt ccc gaa aca aac gag agg aaa aga agg ttc cct agg atc Pro Cys Val Pro Glu Thr Asn Glu Arg Lys Arg Arg Phe Pro Arg Ile 200 205 210			1099
gag ttc ttt ccc gat gaa ccg atg ttg gaa gag aac aaa act tgt gtt Glu Phe Phe Pro Asp Glu Pro Met Leu Glu Glu Asn Lys Thr Cys Val 215 220 225 230			1147
gtt gtg aga gag gaa ggt tct aca agc cct tct tca cac aca aga gag Val Val Arg Glu Glu Gly Ser Thr Ser Pro Ser Ser His Thr Arg Glu 235 240 245			1195
cat caa gtg gaa cag tta gag tca tcg ata gcg att tgg gag aat ctt His Gln Val Glu Gln Leu Glu Ser Ser Ile Ala Ile Trp Glu Asn Leu 250 255 260			1243
gta tcg gat tct tgt gag agt atg tta caa tca aga agt atg atg aca Val Ser Asp Ser Cys Glu Ser Met Leu Gln Ser Arg Ser Met Met Thr 265 270 275			1291
ctt gat gtg gat gaa tca tct act ttt cca gag agc cct cct ctt tct Leu Asp Val Asp Glu Ser Ser Thr Phe Pro Glu Ser Pro Pro Leu Ser 280 285 290			1339
tgc ata cag tta agt gtc gat tca cgt ctc aaa tct cct cct tct cca Cys Ile Gln Leu Ser Val Asp Ser Arg Leu Lys Ser Pro Pro Ser Pro 295 300 305 310			1387
agg atc atc gat atg aac tgt gag ccc gat ggt tcg aaa gaa cag aac Arg Ile Ile Asp Met Asn Cys Glu Pro Asp Gly Ser Lys Glu Gln Asn 315 320 325			1435
act gtt gct gct cct cct cct cct cca gta gca gga gcg aat gat ggc Thr Val Ala Ala Pro Pro Pro Pro Pro Val Ala Gly Ala Asn Asp Gly 330 335 340			1483
ttc tgg cag cag ttt ttc tca gag aat cct ggc tca acc gag caa cgg Phe Trp Gln Gln Phe Phe Ser Glu Asn Pro Gly Ser Thr Glu Gln Arg 345 350 355			1531
gaa gtt caa tta gag agg aaa gac gat aaa gat aaa gcc gga gta cgt Glu Val Gln Leu Glu Arg Lys Asp Asp Lys Asp Lys Ala Gly Val Arg 360 365 370			1579
act gag aaa tgt tgg tgg aat tcg aga aat gtt aat gca att aca gaa Thr Glu Lys Cys Trp Trp Asn Ser Arg Asn Val Asn Ala Ile Thr Glu 375 380 385 390			1627
cag ctt gga cat ctg act tct tca gag aga agt tga tatgtcaaag Gln Leu Gly His Leu Thr Ser Ser Glu Arg Ser 395 400			1673
attaaatttc tagtctgttt tagttacttg taaaataggg tttctcagtt ttattgtttt			1733
cgattccagt acttaggtat gggttcagctg tttattttatc acttgatatga tctttcccag			1793
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aaaa			1857

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 <212> PRT
 <213> Arabidopsis thaliana

MBI15 Sequence Listing.ST25

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Leu Thr Lys Thr Tyr Glu Met Val Asp Asp Ser Ser Ser Asp Ser Ile
20 25 30

Val Ser Trp Ser Gln Ser Asn Lys Ser Phe Ile Val Trp Asn Pro Pro
35 40 45

Glu Phe Ser Arg Asp Leu Leu Pro Arg Phe Phe Lys His Asn Asn Phe
50 55 60

Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ala Asp
65 70 75 80

Pro Glu Gln Trp Glu Phe Ala Asn Asp Asp Phe Val Arg Gly Gln Pro
85 90 95

His Leu Met Lys Asn Ile His Arg Arg Lys Pro Val His Ser His Ser
100 105 110

Leu Pro Asn Leu Gln Ala Gln Leu Asn Pro Leu Thr Asp Ser Glu Arg
115 120 125

Val Arg Met Asn Asn Gln Ile Glu Arg Leu Thr Lys Glu Lys Glu Gly
130 135 140

Leu Leu Glu Glu Leu His Lys Gln Asp Glu Glu Arg Glu Val Phe Glu
145 150 155 160

Met Gln Val Lys Glu Leu Lys Glu Arg Leu Gln His Met Glu Lys Arg
165 170 175

Gln Lys Thr Met Val Ser Phe Val Ser Gln Val Leu Glu Lys Pro Gly
180 185 190

Leu Ala Leu Asn Leu Ser Pro Cys Val Pro Glu Thr Asn Glu Arg Lys
195 200 205

Arg Arg Phe Pro Arg Ile Glu Phe Phe Pro Asp Glu Pro Met Leu Glu
210 215 220

Glu Asn Lys Thr Cys Val Val Val Arg Glu Glu Gly Ser Thr Ser Pro
225 230 235 240

Ser Ser His Thr Arg Glu His Gln Val Glu Gln Leu Glu Ser Ser Ile
245 250 255

Ala Ile Trp Glu Asn Leu Val Ser Asp Ser Cys Glu Ser Met Leu Gln
260 265 270

Ser Arg Ser Met Met Thr Leu Asp Val Asp Glu Ser Ser Thr Phe Pro
275 280 285

MBI15 Sequence Listing.ST25

Glu Ser Pro Pro Leu Ser Cys Ile Gln Leu Ser Val Asp Ser Arg Leu
 290 295 300

Lys Ser Pro Pro Ser Pro Arg Ile Ile Asp Met Asn Cys Glu Pro Asp
 305 310 315 320

Gly Ser Lys Glu Gln Asn Thr Val Ala Ala Pro Pro Pro Pro Val
 325 330 335

Ala Gly Ala Asn Asp Gly Phe Trp Gln Gln Phe Phe Ser Glu Asn Pro
 340 345 350

Gly Ser Thr Glu Gln Arg Glu Val Gln Leu Glu Arg Lys Asp Asp Lys
 355 360 365

Asp Lys Ala Gly Val Arg Thr Glu Lys Cys Trp Trp Asn Ser Arg Asn
 370 375 380

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 <223> G28

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 1 5 10 15
 tcc ata cga cga cac tta cta gga gaa tcg gag ccg ata ctc agt gag 155
 Ser Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu
 20 25 30
 tcg aca gcg agt tcg gtt act caa tct tgt gta acc ggt cag agc att 203
 Ser Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile
 35 40 45
 aaa ccg gtg tac gga cga aac cct agc ttt agc aaa ctg tat cct tgc 251
 Lys Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys
 50 55 60
 ttc acc gag agc tgg gga gat ttg ccg ttg aaa gaa aac gat tct gag 299
 Phe Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu
 65 70 75
 gat atg tta gtt tac ggt atc ctc aac gac gcc ttt cac ggc ggt tgg 347
 Asp Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp
 80 85 90 95
 gag ccg tct tct tcg tct tcc gac gaa gat cgt agc tct ttc ccg agt 395
 Glu Pro Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser
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MBI15 Sequence Listing.ST25

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Val Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro
115 120 125
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Val Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala
130 135 140
aag gga aag cat tat aga gga gtg aga caa agg ccg tgg ggg aaa ttt 539
Lys Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
145 150 155
gcg gcg gag att aga gat ccg gcg aag aac gga gct agg gtt tgg tta 587
Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
160 165 170 175
gga acg ttt gag acg gcg gag gac gcg gcg ttg gct tac gac aga gct 635
Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala
180 185 190
gct ttc agg atg cgt ggt tcc cgc gct ttg ttg aat ttt ccg ttg aga 683
Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
195 200 205
gtt aat tca gga gaa ccc gac ccg gtt cga atc aag tcc aag aga tct 731
Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser
210 215 220
tct ttt tct tct tct aac gag aac gga gct ccg aag aag agg aga acg 779
Ser Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr
225 230 235
gtg gcc gcc ggt ggt gga atg gat aag gga ttg acg gtg aag tgc gag 827
Val Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu
240 245 250 255
gtt gtt gaa gtg gca cgt ggc gat cgt tta ttg gtt tta taa 869
Val Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu
260 265
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<212> PRT
<213> Arabidopsis thaliana

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Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile Lys
35 40 45
Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe
50 55 60
Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp
65 70 75 80
Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu
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MBI15 Sequence Listing.ST25

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 100 105 110

Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val
 115 120 125

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 130 135 140

Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
 145 150 155 160

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
 165 170 175

Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala Ala
 180 185 190

Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val
 195 200 205

Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser
 210 215 220

Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val
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 245 250 255

Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu
 260 265

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 <222> (428) .. (1402)
 <223> G869

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 ctccgatttc atcatcatct tccccatcat cgctgtcttt gaaatcttgt cttctcaacg 180
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 gcttaagacc caaaaggact tggtctagtg ttgaagtctt tggggggtttt cacataaagc 300
 agcaaaagtt ttcttttttc atagttcgct gagagttttg agttttgata ccaaaaaagt 360
 tttgaccttt tagagtgatt ttttgttctt tctgttttct gggatattttt gaggagtggg 420
 ttttaaca atg gtt gcg att aga aag gaa cag tct ttg agt ggt gtt agt 469
 Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser
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 agc gag att aag aag aga gct aag aga aac act cta tcg tcc ctt cct 517

MBI15 Sequence Listing.ST25

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Gln	Glu	Thr	Gln	Pro 35	Leu	Arg	Lys	Val	Arg 40	Ile	Ile	Val	Asn	Asp 45	Pro	
tat	gct	act	gat	gat	tcc	tct	agt	gat	gag	gaa	gag	ctt	aag	gtt	cct	613
Tyr	Ala	Thr	Asp 50	Asp	Ser	Ser	Ser	Asp 55	Glu	Glu	Glu	Leu	Lys 60	Val	Pro	
aag	cca	agg	aaa	atg	aaa	cgt	atc	gtt	cgt	gag	att	aac	ttt	cct	tct	661
Lys	Pro	Arg 65	Lys	Met	Lys	Arg	Ile 70	Val	Arg	Glu	Ile	Asn 75	Phe	Pro	Ser	
atg	gaa	gtt	tct	gaa	cag	cct	tct	gag	agt	tct	tct	cag	gac	agt	act	709
Met	Glu	Val	Ser	Glu	Gln	Pro 85	Ser	Glu	Ser	Ser	Ser	Gln	Asp	Ser	Thr	
80																
aaa	act	gat	ggc	aag	ata	gct	gtg	tca	gct	tct	cct	gct	gtt	cct	agg	757
Lys	Thr	Asp	Gly	Lys	Ile 100	Ala	Val	Ser	Ala	Ser 105	Pro	Ala	Val	Pro	Arg 110	
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Lys	Lys	Pro	Val	Gly 115	Val	Arg	Gln	Arg	Lys 120	Trp	Gly	Lys	Trp	Ala 125	Ala	
gag	att	aga	gat	cct	att	aag	aaa	act	agg	act	tgg	ttg	ggc	act	ttt	853
Glu	Ile	Arg	Asp 130	Pro	Ile	Lys	Lys	Thr 135	Arg	Thr	Trp	Leu	Gly 140	Thr	Phe	
gat	act	ctt	gaa	gaa	gct	gct	aaa	gct	tat	gat	gct	aag	aag	ctt	gag	901
Asp	Thr	Leu 145	Glu	Glu	Ala	Ala	Lys 150	Ala	Tyr	Asp	Ala	Lys 155	Lys	Leu	Glu	
ttt	gat	gct	att	gtt	gct	gga	aat	gtg	tcc	act	act	aaa	cgt	gat	gtt	949
Phe	Asp	Ala	Ile	Val	Ala	Gly 165	Asn	Val	Ser	Thr	Thr	Lys	Arg	Asp	Val	
160																
tct	tca	tct	gag	act	agc	caa	tgc	tct	cgt	tct	tca	cct	gtt	gtt	cct	997
Ser	Ser	Ser	Glu	Thr	Ser 180	Gln	Cys	Ser	Arg 185	Ser	Ser	Pro	Val	Val	Pro 190	
175																
gtt	gag	caa	gat	gac	act	tct	gca	tca	gct	ctc	act	tgt	gtc	aac	aac	1045
Val	Glu	Gln	Asp	Asp 195	Thr	Ser	Ala	Ser	Ala 200	Leu	Thr	Cys	Val	Asn 205	Asn	
cct	gat	gac	gtc	tcg	acc	gtt	gct	cca	act	gct	cca	act	cca	aat	gtt	1093
Pro	Asp	Asp	Val 210	Ser	Thr	Val	Ala	Pro 215	Thr	Ala	Pro	Thr	Pro	Asn 220	Val	
cct	gct	ggc	gga	aac	aag	gaa	acg	ttg	ttc	gat	ttc	gac	ttt	act	aat	1141
Pro	Ala	Gly 225	Gly	Asn	Lys	Glu	Thr 230	Leu	Phe	Asp	Phe	Asp 235	Phe	Thr	Asn	
cta	cag	atc	cct	gat	ttt	ggc	ttc	ttg	gca	gag	gag	caa	caa	gac	cta	1189
Leu	Gln	Ile	Pro	Asp	Phe	Gly 245	Phe	Leu	Ala	Glu	Glu	Gln	Gln	Asp	Leu	
240																
gac	ttc	gat	tgt	ttc	ctc	gcg	gat	gat	cag	ttt	gat	gat	ttc	ggc	ttg	1237
Asp	Phe	Asp	Cys	Phe	Leu	Ala	Asp	Asp	Gln 265	Phe	Asp	Asp	Phe	Gly	Leu 270	
255																
ctt	gat	gac	att	caa	gga	ttc	gaa	gat	aac	ggc	cca	agt	gcg	tta	cca	1285
Leu	Asp	Asp	Ile	Gln 275	Gly	Phe	Glu	Asp	Asn 280	Gly	Pro	Ser	Ala	Leu 285	Pro	
gat	ttc	gac	ttt	gcg	gat	gtt	gaa	gat	ctt	cag	cta	gct	gac	tct	agt	1333
Asp	Phe	Asp	Phe	Ala	Asp	Val	Glu	Asp 295	Leu	Gln	Leu	Ala	Asp	Ser	Ser	
290																
ttc	ggc	ttc	ctt	gat	caa	ctt	gct	cct	atc	aac	atc	tct	tgc	cca	tta	1381
Phe	Gly	Phe	Leu	Asp	Gln	Leu	Ala 310	Pro	Ile	Asn	Ile	Ser 315	Cys	Pro	Leu	
305																

MBI15 Sequence Listing.ST25

aaa agt ttt gca gct tca tag gatcttgctt agtaatgtta agtgagaaga 1432
 Lys Ser Phe Ala Ala Ser
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attgtagtaa gatcttaaga cataaagccg ggttttgcaa ttaggaatcg agttttaatg 1552

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<212> PRT

<213> Arabidopsis thaliana

<400> 12

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Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro Gln Glu
 20 25 30

Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro Tyr Ala
 35 40 45

Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro
 50 55 60

Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser Met Glu
 65 70 75 80

Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr
 85 90 95

Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys
 100 105 110

Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala Glu Ile
 115 120 125

Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe Asp Thr
 130 135 140

Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu Phe Asp
 145 150 155 160

Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser
 165 170 175

Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu
 180 185 190

Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp
 195 200 205

Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala
 210 215 220

Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln

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225                               230                               235                               240
Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe
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Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp
                260                               265                               270

Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe
                275                               280                               285

Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly
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Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu Lys Ser
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Phe Ala Ala Ser

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Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser				5					10					15			
cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat																	96
Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His			20					25					30				
tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg																	144
Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly			35				40					45					
aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag																	192
Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys		50				55					60						
agg gat atg att agt gca gaa gaa gaa gag act atc ttg acg ttt cat																	240
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His					70					75				80			
tct ccc ttg ggt aac aag tgg tcg caa ata gct aaa ttc tta ccg gga																	288
Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly				85				90						95			
aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag																	336
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys			100					105					110				
aaa tgg ctc aag tct cag agc tta caa gat gca aaa tct att tcc cct																	384
Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro		115					120					125					
cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg																	432
Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro		130				135					140						

MBI15 Sequence Listing.ST25

gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag 480
 Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
 145 150 155 160

 aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat 528
 Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
 165 170 175

 caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg 576
 Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
 180 185 190

 ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac 624
 Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
 195 200 205

 tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat 672
 Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
 210 215 220

 gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc 720
 Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
 225 230 235 240

 aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt 768
 Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
 245 250 255

 aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct 816
 Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
 260 265 270

 tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta 862
 Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr
 275 280

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<210> 14
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 14

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 Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
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 Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
 35 40 45

 Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
 50 55 60

 Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
 65 70 75 80

 Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
 85 90 95

 Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
 100 105 110

 Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro

MBI15 Sequence Listing.ST25

115 120 125

Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
130 135 140

Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
145 150 155 160

Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
165 170 175

Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
180 185 190

Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
195 200 205

Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
210 215 220

Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225 230 235 240

Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
245 250 255

Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
260 265 270

Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
275 280

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<212> DNA
<213> Arabidopsis thaliana

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<223> G409

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atgatgggat ttgtatctg cccgttgag tcacctgcga gattactatg gagtacaagc 180
ttcttcgcgc ataagatcat gatcttctaa tccttcctac ttcttcccat ctttttaatc 240
atcttctcgc tatctctgct tcctctttct ctctgtttcc tctttctcag aactcagaag 300
tagttgttgt tttatttctg ttgatcaaaa atg gaa tcc aat tcg ttt ttc ttc 354
Met Glu Ser Asn Ser Phe Phe Phe
1 5
gat cca tct gct tca cac ggc aac agc atg ttc ttc ctt ggg aat ctc 402
Asp Pro Ser Ala Ser His Gly Asn Ser Met Phe Phe Leu Gly Asn Leu
10 15 20
aat ccc gtc gtc caa gga gga gga gca aga tcg atg atg aac atg gag 450
Asn Pro Val Val Gln Gly Gly Gly Ala Arg Ser Met Met Asn Met Glu

MBI15 Sequence Listing.ST25

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Glu Thr Ser Lys Arg Arg Pro Phe Phe Ser Ser Pro Glu Asp Leu Tyr	45	50	55	
gac gat gac ttt tac gac gac cag ttg cct gaa aag aag cgt cgc ctc				546
Asp Asp Asp Phe Tyr Asp Asp Gln Leu Pro Glu Lys Lys Arg Arg Leu	60	65	70	
act acc gaa caa gtg cat ctg ctg gag aaa agc ttc gag aca gag aac				594
Thr Thr Glu Gln Val His Leu Leu Glu Lys Ser Phe Glu Thr Glu Asn	75	80	85	
aag cta gag cct gaa cgc aag act cag ctt gcc aag aag ctt ggt cta				642
Lys Leu Glu Pro Glu Arg Lys Thr Gln Leu Ala Lys Lys Leu Gly Leu	90	95	100	
cag cca agg caa gtg gct gtc tgg ttt cag aat cgc cga gct cgt tgg				690
Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp	105	110	115	120
aaa aca aaa cag ctt gag aga gac tac gat ctt ctc aag tcc act tac				738
Lys Thr Lys Gln Leu Glu Arg Asp Tyr Asp Leu Leu Lys Ser Thr Tyr	125	130	135	
gac caa ctt ctt tct aac tac gac tcc atc gtc atg gac aac gat aag				786
Asp Gln Leu Leu Ser Asn Tyr Asp Ser Ile Val Met Asp Asn Asp Lys	140	145	150	
ctc aga tcc gag gtt act tcc ctg acc gaa aag ctt cag ggc aaa caa				834
Leu Arg Ser Glu Val Thr Ser Leu Thr Glu Lys Leu Gln Gly Lys Gln	155	160	165	
gag aca gct aat gaa cca cct ggt caa gtg ccc gaa cca aac caa ctt				882
Glu Thr Ala Asn Glu Pro Pro Gly Gln Val Pro Glu Pro Asn Gln Leu	170	175	180	
gat ccg gtt tac att aat gcg gca gca atc aaa acc gag gac cgg tta				930
Asp Pro Val Tyr Ile Asn Ala Ala Ala Ile Lys Thr Glu Asp Arg Leu	185	190	195	200
agt tca ggg agc gtt ggg agc gcg gta cta gac gac gac gca cct caa				978
Ser Ser Gly Ser Val Gly Ser Ala Val Leu Asp Asp Asp Ala Pro Gln	205	210	215	
cta cta gac agc tgt gac tct tac ttc cca agc atc gta ccc atc caa				1026
Leu Leu Asp Ser Cys Asp Ser Tyr Phe Pro Ser Ile Val Pro Ile Gln	220	225	230	
gac aac agc aac gcc agt gat cat gac aat gac cgg agc tgt ttc gcc				1074
Asp Asn Ser Asn Ala Ser Asp His Asp Asn Asp Arg Ser Cys Phe Ala	235	240	245	
gac gtc ttt gtg ccc acc act tca ccg tcg cac gat cat cac ggt gaa				1122
Asp Val Phe Val Pro Thr Thr Ser Pro Ser His Asp His His Gly Glu	250	255	260	
tca ttg gct ttc tgg gga tgg cct tag aaaaccactc tgataataaa				1169
Ser Leu Ala Phe Trp Gly Trp Pro	265	270		
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tgactcgtgg aataattccg ctgttcaacg gtatttttat cagttgcatt atatgctttt				1289
atgaaaaaaaaaaa				1302

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 <213> Arabidopsis thaliana

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MBI15 Sequence Listing.ST25

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 20 25 30

Ala Arg Ser Met Met Asn Met Glu Glu Thr Ser Lys Arg Arg Pro Phe
 35 40 45

Phe Ser Ser Pro Glu Asp Leu Tyr Asp Asp Asp Phe Tyr Asp Asp Gln
 50 55 60

Leu Pro Glu Lys Lys Arg Arg Leu Thr Thr Glu Gln Val His Leu Leu
 65 70 75 80

Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr
 85 90 95

Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp
 100 105 110

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp
 115 120 125

Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp
 130 135 140

Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu
 145 150 155 160

Thr Glu Lys Leu Gln Gly Lys Gln Glu Thr Ala Asn Glu Pro Pro Gly
 165 170 175

Gln Val Pro Glu Pro Asn Gln Leu Asp Pro Val Tyr Ile Asn Ala Ala
 180 185 190

Ala Ile Lys Thr Glu Asp Arg Leu Ser Ser Gly Ser Val Gly Ser Ala
 195 200 205

Val Leu Asp Asp Asp Ala Pro Gln Leu Leu Asp Ser Cys Asp Ser Tyr
 210 215 220

Phe Pro Ser Ile Val Pro Ile Gln Asp Asn Ser Asn Ala Ser Asp His
 225 230 235 240

Asp Asn Asp Arg Ser Cys Phe Ala Asp Val Phe Val Pro Thr Thr Ser
 245 250 255

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 260 265 270

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MBI15 Sequence Listing.ST25

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 Met Gly Ile Thr
 1
 aaa act tct cct aat act aca att ctc ttg aag act ttt cac aat aat 162
 Lys Thr Ser Pro Asn Thr Thr Ile Leu Leu Lys Thr Phe His Asn Asn
 5 10 15 20
 tct atg tcc caa gat tat cat cat cat cat cat cat aat caa cac caa 210
 Ser Met Ser Gln Asp Tyr His His His His His His Asn Gln His Gln
 25 30 35
 gga ggt atc ttc aac ttc tct aat gga ttc gac cga tca gat tct ccc 258
 Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg Ser Asp Ser Pro
 40 45 50
 aat tta aca act cag cag aag caa gag cat caa agg gta gag atg gac 306
 Asn Leu Thr Thr Gln Gln Lys Gln Glu His Gln Arg Val Glu Met Asp
 55 60 65
 gag gaa tct tca gtc gcc gga ggt agg att ccg gtc tac gaa tca gcc 354
 Glu Glu Ser Ser Val Ala Gly Gly Arg Ile Pro Val Tyr Glu Ser Ala
 70 75 80
 ggt atg tta tcc gaa atg ttt aat ttc ccc gga agc agc ggt gga gga 402
 Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser Ser Gly Gly Gly
 85 90 95 100
 aga gat ctc gac ctc ggc caa tct ttc cgg tca aat agg cag ttg ctt 450
 Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn Arg Gln Leu Leu
 105 110 115
 gag gag caa cat cag aat att ccg gct atg aat gct acg gat tca gcc 498
 Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala Thr Asp Ser Ala
 120 125 130
 acc gcc acc gca gcc gcc atg cag tta ttc ttg atg aat cca ccg cca 546
 Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met Asn Pro Pro Pro
 135 140 145
 ccg caa caa cca ccg tct ccg tca tcc aca act tcc cca agg agc cac 594
 Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser Pro Arg Ser His
 150 155 160
 cac aat tct tca act ctt cac atg tta ctt cca agt cca tcc acc aac 642
 His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser Pro Ser Thr Asn
 165 170 175 180
 aca act cac cat cag aac tac act aat cat atg tct atg cat cag ctt 690
 Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser Met His Gln Leu
 185 190 195
 cca cat cag cat cac caa cag ata tcg acg tgg cag tct tct ccc gat 738
 Pro His Gln His His Gln Gln Ile Ser Thr Trp Gln Ser Ser Pro Asp
 200 205 210
 cat cat cat cat cat cac aac agc caa acg gag att ggg acc gtc cac 786
 His His His His His His Asn Ser Gln Thr Glu Ile Gly Thr Val His
 215 220 225
 gtg gaa aac agc gga gga cac gga gga caa ggc ttg tcc tta tct ctc 834
 Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu Ser Leu Ser Leu
 230 235 240
 tca tcg tct tta gag gct gca gca aaa gcg gaa gag tat aga aac att 882
 Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Asn Ile
 245 250 255 260

MBI15 Sequence Listing.ST25

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tta aac caa ttc cga tca tct ccg gct gct tct tcc tct tcc atg gca Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser Ser Ser Met Ala 295 300 305	1026
gcg gtc aat atc tta aga aac tcg agg tac aca acg gcc gcg caa gag Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr Ala Ala Gln Glu 310 315 320	1074
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aaa ctt ggg aac agc tca aac cct aat act tgc ggt ggt gat ggt ggt Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly Gly Asp Gly Gly 345 350 355	1170
ggc agc tct cct tcg tcg gcc gga gca aac aag gag cat cct cct tta Gly Ser Ser Pro Ser Ser Ala Gly Ala Asn Lys Glu His Pro Pro Leu 360 365 370	1218
tcg gcg tct gat cgg att gag cat caa aga agg aaa gtg aaa cta ctc Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys Val Lys Leu Leu 375 380 385	1266
acc atg ctt gaa gag gtg gac cga cgg tac aac cat tac tgc gag caa Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln 390 395 400	1314
atg cag atg gtt gtg aac tct ttc gac ata gta atg ggc cac ggt gcg Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met Gly His Gly Ala 405 410 415 420	1362
gca tta ccg tac acc gca ttg gct caa aaa gct atg tca aga cat ttt Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met Ser Arg His Phe 425 430 435	1410
aga tgc ctt aaa gat gca gtt gcg gct cag ctt aag cag agt tgc gaa Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys Gln Ser Cys Glu 440 445 450	1458
ctt ctt ggg gac aaa gat gca gcg gga atc tct tct tcc ggg tta aca Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser Ser Gly Leu Thr 455 460 465	1506
aaa ggt gaa act ccg cgt ttg cgt ttg cta gag caa agt ttg cgt cag Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln 470 475 480	1554
caa cgt gcg ttt cat caa atg ggt atg atg gaa caa gaa gct tgg cgg Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln Glu Ala Trp Arg 485 490 495 500	1602
cca caa cgc ggt ttg cct gaa cgc tcc gtc aat ata ctt aga gct tgg Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile Leu Arg Ala Trp 505 510 515	1650
ctc ttc gaa cat ttc ctt cac ccg tat cca agt gat gca gat aaa cac Leu Phe Glu His Phe Leu His Pro Tyr Pro Ser Asp Ala Asp Lys His 520 525 530	1698
cta ttg gct cga cag act ggt tta tcc aga aat cag gta tca aat tgg Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp 535 540 545	1746
ttc ata aat gct agg gtt cgt tta tgg aaa cca atg gtg gaa gaa atg Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met 550 555	1794

MBI15 Sequence Listing.ST25

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tac caa caa gaa tca	aaa gaa aga gaa aga gaa gag gaa tta gaa gag		1842
Tyr Gln Gln Glu Ser	Lys Glu Arg Glu Arg Glu Glu Glu Leu Glu Glu		
565	570 575 580		
aac gaa gaa gat caa	gaa aca aaa aac agc aac gac gac aag agc aca		1890
Asn Glu Glu Asp Gln	Glu Thr Lys Asn Ser Asn Asp Asp Lys Ser Thr		
	585 590 595		
aaa tcc aac aac aat	gaa agc aac ttc act gcc gtt cgg acc act tca		1938
Lys Ser Asn Asn Asn	Glu Ser Asn Phe Thr Ala Val Arg Thr Thr Ser		
	600 605 610		
caa act cca acg aca	acc gca cca gac gca tca gac gca gac gca gca		1986
Gln Thr Pro Thr Thr	Thr Ala Pro Asp Ala Ser Asp Ala Asp Ala Ala		
	615 620 625		
gta gcg aca ggc cac	cgt cta aga tcc aac att aat gct tac gaa aac		2034
Val Ala Thr Gly His	Arg Leu Arg Ser Asn Ile Asn Ala Tyr Glu Asn		
	630 635 640		
gac gct tca tca ctt	cta ctc cct tcc tct tat tcc aac gcc gcc gct		2082
Asp Ala Ser Ser Leu	Leu Leu Pro Ser Ser Tyr Ser Asn Ala Ala Ala		
	645 650 655 660		
cct gcc gct gtt tct	gac gac ttg aat tct cgt tac ggt ggc tca gac		2130
Pro Ala Ala Val Ser	Asp Asp Leu Asn Ser Arg Tyr Gly Gly Ser Asp		
	665 670 675		
gcg ttt tcc gcc gtt	gcc acg tgt caa caa agt gta ggt ggg ttc gat		2178
Ala Phe Ser Ala Val	Ala Thr Cys Gln Gln Ser Val Gly Gly Phe Asp		
	680 685 690		
gat gct gac atg gat	ggg gtt aac gtt ata agg ttt ggg aca aac cct		2226
Asp Ala Asp Met Asp	Gly Val Asn Val Ile Arg Phe Gly Thr Asn Pro		
	695 700 705		
act ggt gac gtg tct	ctc acg ctt ggt tta cgc cac gct gga aac atg		2274
Thr Gly Asp Val Ser	Leu Thr Leu Gly Leu Arg His Ala Gly Asn Met		
	710 715 720		
cct gac aaa gac gct	tct ttc tgc gtt aga gag ttt ggg ggt ttt tag		2322
Pro Asp Lys Asp Ala	Ser Phe Cys Val Arg Glu Phe Gly Gly Phe		
	725 730 735		
tttgcttttg tcaactccatt	taattaatta attatagttt tccattctta cttatttttaa		2382
ttgaaaatct atttttgtct	cttaaaagtc caaacaatac attagtctag cctcctctg		2442
ctttttttttt tctatctcgt	gaagagaaga aaacgatacg taaatccctt cgaaaactaa		2502
tgtacgttgt acgacttatt	gttttcataa aaaaaaaaaa aaa		2545

<210> 18
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<400> 18

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Phe His Asn Asn Ser Met Ser Gln Asp Tyr His His His His His His
20 25 30

Asn Gln His Gln Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg
35 40 45

Ser Asp Ser Pro Asn Leu Thr Thr Gln Gln Lys Gln Glu His Gln Arg

MBI15 Sequence Listing.ST25

50	55	60	
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Tyr Glu Ser Ala Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser			
	85	90	95
Ser Gly Gly Gly Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn			
	100	105	110
Arg Gln Leu Leu Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala			
	115	120	125
Thr Asp Ser Ala Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met			
	130	135	140
Asn Pro Pro Pro Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser			
145	150	155	160
Pro Arg Ser His His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser			
	165	170	175
Pro Ser Thr Asn Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser			
	180	185	190
Met His Gln Leu Pro His Gln His His Gln Gln Ile Ser Thr Trp Gln			
	195	200	205
Ser Ser Pro Asp His His His His His His Asn Ser Gln Thr Glu Ile			
	210	215	220
Gly Thr Val His Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu			
225	230	235	240
Ser Leu Ser Leu Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu			
	245	250	255
Tyr Arg Asn Ile Tyr Tyr Gly Ala Asn Ser Ser Asn Ala Ser Pro His			
	260	265	270
His Gln Tyr Asn Gln Phe Lys Thr Leu Leu Ala Asn Ser Ser Gln His			
	275	280	285
His His Gln Val Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser			
	290	295	300
Ser Ser Met Ala Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr			
305	310	315	320
Ala Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser Val Gly Arg Gly Phe			
	325	330	335
Leu Lys Lys Asn Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly			
	340	345	350

MBI15 Sequence Listing.ST25

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 355 360 365
 His Pro Pro Leu Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys
 370 375 380
 Val Lys Leu Leu Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His
 385 390 395 400
 Tyr Cys Glu Gln Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met
 405 410 415
 Gly His Gly Ala Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met
 420 425 430
 Ser Arg His Phe Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys
 435 440 445
 Gln Ser Cys Glu Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser
 450 455 460
 Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln
 465 470 475 480
 Ser Leu Arg Gln Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln
 485 490 495
 Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile
 500 505 510
 Leu Arg Ala Trp Leu Phe Glu His Phe Leu His Pro Tyr Pro Ser Asp
 515 520 525
 Ala Asp Lys His Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln
 530 535 540
 Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met
 545 550 555 560
 Val Glu Glu Met Tyr Gln Gln Glu Ser Lys Glu Arg Glu Arg Glu Glu
 565 570 575
 Glu Leu Glu Glu Asn Glu Glu Asp Gln Glu Thr Lys Asn Ser Asn Asp
 580 585 590
 Asp Lys Ser Thr Lys Ser Asn Asn Asn Glu Ser Asn Phe Thr Ala Val
 595 600 605
 Arg Thr Thr Ser Gln Thr Pro Thr Thr Thr Ala Pro Asp Ala Ser Asp
 610 615 620
 Ala Asp Ala Ala Val Ala Thr Gly His Arg Leu Arg Ser Asn Ile Asn
 625 630 635 640
 Ala Tyr Glu Asn Asp Ala Ser Ser Leu Leu Leu Pro Ser Ser Tyr Ser
 645 650 655

MBI15 Sequence Listing.ST25

Asn Ala Ala Ala Pro Ala Ala Val Ser Asp Asp Leu Asn Ser Arg Tyr
660 665 670

Gly Gly Ser Asp Ala Phe Ser Ala Val Ala Thr Cys Gln Gln Ser Val
675 680 685

Gly Gly Phe Asp Asp Ala Asp Met Asp Gly Val Asn Val Ile Arg Phe
690 695 700

Gly Thr Asn Pro Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His
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Ala Gly Asn Met Pro Asp Lys Asp Ala Ser Phe Cys Val Arg Glu Phe
725 730 735

Gly Gly Phe

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<223> G591

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tcaaagtctc tgtcttttagc tcaaacc atg gct agt aac aac cct cac gac aac 114
Met Ala Ser Asn Asn Pro His Asp Asn
1 5
ctt tct gac caa act cct tct gat gat ttc ttc gag caa atc ctc ggc 162
Leu Ser Asp Gln Thr Pro Ser Asp Asp Phe Phe Glu Gln Ile Leu Gly
10 15 20 25
ctt cct aac ttc tca gcc tct tct gcc gcc ggt tta tct gga gtt gac 210
Leu Pro Asn Phe Ser Ala Ser Ser Ala Ala Gly Leu Ser Gly Val Asp
30 35 40
gga gga tta ggt ggt gga gca ccg cct atg atg ctg cag ttg ggt tcc 258
Gly Gly Leu Gly Gly Gly Ala Pro Pro Met Met Leu Gln Leu Gly Ser
45 50 55
gga gaa gaa gga agt cac atg ggt ggc tta gga gga agt gga cca act 306
Gly Glu Glu Gly Ser His Met Gly Gly Leu Gly Gly Ser Gly Pro Thr
60 65 70
ggg ttt cac aat cag atg ttt cct ttg ggg tta agt ctt gat caa ggg 354
Gly Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly
75 80 85
aaa gga cct ggg ttt ctt aga cct gaa gga gga cat gga agt ggg aaa 402
Lys Gly Pro Gly Phe Leu Arg Pro Glu Gly Gly His Gly Ser Gly Lys
90 95 100 105
aga ttc tca gat gat gtt gtt gat aat cga tgt tct tct atg aaa cct 450
Arg Phe Ser Asp Asp Val Val Asp Asn Arg Cys Ser Ser Met Lys Pro
110 115 120
gtt ttc cac ggg cag cct atg caa cag cca cct cca tcg gcc cca cat 498
Val Phe His Gly Gln Pro Met Gln Gln Pro Pro Pro Ser Ala Pro His
125 130 135

MBI15 Sequence Listing.ST25

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 Gln Pro Thr Ser Ile Arg Pro Arg Val Arg Ala Arg Arg Gly Gln Ala
 140 145 150

act gat cca cat agc atc gct gag cgg cta cgt aga gaa aga ata gca 594
 Thr Asp Pro His Ser Ile Ala Glu Arg Leu Arg Arg Glu Arg Ile Ala
 155 160 165

gaa cgg atc agg gcg ctg cag gaa ctt gta cct act gtg aac aag acc 642
 Glu Arg Ile Arg Ala Leu Gln Glu Leu Val Pro Thr Val Asn Lys Thr
 170 175 180 185

gat aga gct gct atg atc gat gag att gtc gat tat gta aag ttt ctc 690
 Asp Arg Ala Ala Met Ile Asp Glu Ile Val Asp Tyr Val Lys Phe Leu
 190 195 200

agg ctc caa gtc aag gtt ttg agc atg aac cga ctt ggt gga gcc ggt 738
 Arg Leu Gln Val Lys Val Leu Ser Met Asn Arg Leu Gly Gly Ala Gly
 205 210 215

gcg gtt gct cca ctt gtt act gat atg cct ctt tca tca tca gtt gag 786
 Ala Val Ala Pro Leu Val Thr Asp Met Pro Leu Ser Ser Ser Val Glu
 220 225 230

gat gaa acg ggt gag ggt gga agg act ccg caa cca gcg tgg gag aaa 834
 Asp Glu Thr Gly Glu Gly Gly Arg Thr Pro Gln Pro Ala Trp Glu Lys
 235 240 245

tgg tct aac gat ggg act gaa cgt caa gtg gct aaa ctg atg gaa gag 882
 Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu
 250 255 260 265

aac gtt gga gcc gcg atg cag ctt ctt caa tca aag gct ctt tgt atg 930
 Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Met
 270 275 280

atg cca atc tca ttg gca atg gca att tac cat tct caa cct ccg gat 978
 Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp
 285 290 295

aca tct tca gtg gtc aag cct gag aac aat cct cca cag tag 1020
 Thr Ser Ser Val Val Lys Pro Glu Asn Asn Pro Pro Gln
 300 305 310

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gctctaataga ctctgggttct ttctctcctc tctcaccgac ttgaaaggta aaaaagtga 1140

aaaggctttg tagatggaat caatgtagga tttgcagtag agggcaaaaa aatgtcatat 1200

agctcaattg atcaagtctt aaaaaaaaaa aaaaaaaaaa 1240

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 <212> PRT
 <213> Arabidopsis thaliana

<400> 20

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 1 5 10 15

Asp Asp Phe Phe Glu Gln Ile Leu Gly Leu Pro Asn Phe Ser Ala Ser
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Ser Ala Ala Gly Leu Ser Gly Val Asp Gly Gly Leu Gly Gly Gly Ala
 35 40 45

Pro Pro Met Met Leu Gln Leu Gly Ser Gly Glu Glu Gly Ser His Met
 50 55 60

MBI15 Sequence Listing.ST25

Gly Gly Leu Gly Gly Ser Gly Pro Thr Gly Phe His Asn Gln Met Phe
 65 70 75 80
 Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly Pro Gly Phe Leu Arg
 85 90 95
 Pro Glu Gly Gly His Gly Ser Gly Lys Arg Phe Ser Asp Asp Val Val
 100 105 110
 Asp Asn Arg Cys Ser Ser Met Lys Pro Val Phe His Gly Gln Pro Met
 115 120 125
 Gln Gln Pro Pro Pro Ser Ala Pro His Gln Pro Thr Ser Ile Arg Pro
 130 135 140
 Arg Val Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala
 145 150 155 160
 Glu Arg Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ala Leu Gln
 165 170 175
 Glu Leu Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp
 180 185 190
 Glu Ile Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu
 195 200 205
 Ser Met Asn Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr
 210 215 220
 Asp Met Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gly Glu Gly Gly
 225 230 235 240
 Arg Thr Pro Gln Pro Ala Trp Glu Lys Trp Ser Asn Asp Gly Thr Glu
 245 250 255
 Arg Gln Val Ala Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln
 260 265 270
 Leu Leu Gln Ser Lys Ala Leu Cys Met Met Pro Ile Ser Leu Ala Met
 275 280 285
 Ala Ile Tyr His Ser Gln Pro Pro Asp Thr Ser Ser Val Val Lys Pro
 290 295 300
 Glu Asn Asn Pro Pro Gln
 305 310

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 <222> (109)..(966)
 <223> G525

MBI15 Sequence Listing.ST25

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                               Met Asp Tyr
                               1

gag gca tca aga atc gtc gaa atg gta gaa gat gaa gaa cat ata gat      165
Glu Ala Ser Arg Ile Val Glu Met Val Glu Asp Glu Glu His Ile Asp
5                               10                               15

cta cca cca gga ttc aga ttt cac cct act gat gaa gaa ctc ata act      213
Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr
20                               25                               30                               35

cac tac ctc aaa cca aag gtt ttc aac act ttc ttc tct gct act gcc      261
His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser Ala Thr Ala
40                               45                               50

att ggt gaa gtt gat ctc aac aag att gag cct tgg gac tta cca tgg      309
Ile Gly Glu Val Asp Leu Asn Lys Ile Glu Pro Trp Asp Leu Pro Trp
55                               60                               65

aag gct aag atg gga gaa aaa gaa tgg tat ttc ttc tgt gtg aga gac      357
Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp
70                               75                               80

cgg aaa tac ccg acc ggt tta agg aca aac cgg gcg aca gaa gcc ggt      405
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly
85                               90                               95

tat tgg aaa gcc aca gga aaa gac aaa gag ata ttc aag gga aaa tca      453
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Ser
100                               105                               110                               115

ctt gtg ggt atg aag aaa act ttg gtt ttc tat aaa gga aga gct cct      501
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro
120                               125                               130

aaa gga gtt aaa acc aat tgg gtt atg cat gaa tat cgt tta gaa ggc      549
Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly
135                               140                               145

aaa tat tgt att gaa aat ctt ccc caa aca gct aag aac gaa tgg gtt      597
Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn Glu Trp Val
150                               155                               160

ata tgt cgt gtt ttc caa aaa cgt gcc gat ggt aca aag gtt cca atg      645
Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys Val Pro Met
165                               170                               175

tca atg ctt gat cca cac att aac cga atg gaa cca gcc ggt tta cct      693
Ser Met Leu Asp Pro His Ile Asn Arg Met Glu Pro Ala Gly Leu Pro
180                               185                               190                               195

tcg tta atg gat tgt tct caa cga gac tcc ttc acc ggt tcg tcg tct      741
Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly Ser Ser Ser
200                               205                               210

cac gtg acc tgc ttc tcc gac caa gaa acc gaa gac aaa aga ctt gtc      789
His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys Arg Leu Val
215                               220                               225

cac gag tcc aaa gac ggt ttt ggt tct ctg ttt tac tcg gat cct ctg      837
His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser Asp Pro Leu
230                               235                               240

ttt tta caa gac aat tat tcg cta atg aag ctg ttg ctt gac ggt caa      885
Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu Asp Gly Gln
245                               250                               255

gaa act caa ttc tcc ggc aaa cct ttc gac ggt cgt gat tcg tcc ggt      933
Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp Ser Ser Gly
260                               265                               270                               275

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MBI15 Sequence Listing.ST25

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 Thr Glu Glu Leu Asp Cys Val Trp Asn Phe
 280 285

gacttgtagt agtcatgtgt tcgtgtgtgt gaatgaatat tcttgttaca tttttttgta 1046

aaaaaggaga aaaaaatatg ctagaaagtc aattgctttt gttatgtagc attagtgttt 1106

tttatgtact caatagactt cctaattaaa taaaaatctt aatttatttg ccaaaaaaaaa 1166

aaaaaaaaaa aaa 1179

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 <211> 285
 <212> PRT
 <213> Arabidopsis thaliana

<400> 22

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His Ile Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu
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Leu Ile Thr His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser
 35 40 45

Ala Thr Ala Ile Gly Glu Val Asp Leu Asn Lys Ile Glu Pro Trp Asp
 50 55 60

Leu Pro Trp Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys
 65 70 75 80

Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr
 85 90 95

Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys
 100 105 110

Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly
 115 120 125

Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg
 130 135 140

Leu Glu Gly Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn
 145 150 155 160

Glu Trp Val Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys
 165 170 175

Val Pro Met Ser Met Leu Asp Pro His Ile Asn Arg Met Glu Pro Ala
 180 185 190

Gly Leu Pro Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly
 195 200 205

Ser Ser Ser His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys
 210 215 220

MBI15 Sequence Listing.ST25

Arg Leu Val His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser
225 230 235 240

Asp Pro Leu Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu
245 250 255

Asp Gly Gln Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp
260 265 270

Ser Ser Gly Thr Glu Glu Leu Asp Cys Val Trp Asn Phe
275 280 285

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<212> DNA
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<223> G545

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Met
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Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro
5 10 15

ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag 153
Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys
20 25 30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc 201
Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu
35 40 45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac 249
Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp
50 55 60 65

aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag 297
Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys
70 75 80

tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt 345
Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly
85 90 95

cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga 393
His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly
100 105 110

gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act 441
Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Ser Ala Val Thr
115 120 125

act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt 489
Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe
130 135 140 145

cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga 537
Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly
150 155 160

aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg 585

MBI15 Sequence Listing.ST25

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 tcc act agc cac gtt agc agt agc cac cgt ggg ttt gac ctc aac atc 633
 Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile
 180 185 190
 cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg 681
 Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met
 195 200 205
 agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt 729
 Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu
 210 215 220 225
 caa ctt taa ggaaatttac ttagacgata agatttcgtt tgtatactgt 778
 Gln Leu
 tgagagttgt gtaggaattt gttgactgta cataccaaatt tggactttga ctgattccaa 838
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 Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
 35 40 45
 Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
 50 55 60
 Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
 65 70 75 80
 Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
 85 90 95
 Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
 100 105 110
 Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
 115 120 125
 Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
 130 135 140
 Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
 145 150 155 160
 Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
 165 170 175

MBI15 Sequence Listing.ST25

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
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Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
210 215 220

Leu Gln Leu
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<212> DNA
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<222> (282)..(920)
<223> G865

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cacacctatt attctcttgg tgtgtttgtg tgttacatat acgtgtgagt acatactttg 180
ttgtaaaagt ggatcggagg tatggaaagg gaccggttcc accggaaaca tcggcggcgg 240
cggatgataa ttcgtcttgg aacgagactg atgtcaccgc c atg gtc tcc gct ctc 296
Met Val Ser Ala Leu
1 5
agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt 344
Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro Val Lys Gln Glu Leu
10 15 20
gat aaa tcg gat caa cat caa cca gac caa gat caa cca aga aga aga 392
Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp Gln Pro Arg Arg Arg
25 30 35
cac tat aga ggc gta agg cag aga cca tgg ggt aaa tgg gcg gca gaa 440
His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
40 45 50
atc cgc gat cca aag aaa gca gcc cgt gtc tgg ctc ggg act ttc gag 488
Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
55 60 65
acg gca gag gaa gct gct tta gcc tat gac cga gct gcc ctc aaa ttc 536
Thr Ala Glu Glu Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe
70 75 80 85
aaa ggc acc aag gct aaa ctg aac ttc cct gaa cgg gtc caa ggc cct 584
Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro
90 95 100
act acc acc aca acc att tct cat gca cca aga gga gtt agt gaa tcc 632
Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser
105 110 115
atg aac tca cct cct cct cga cct ggt cca cct tca act act act act 680
Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro Ser Thr Thr Thr Thr
120 125 130
tcg tgg cca atg act tat aac cag gac ata ctt caa tac gct cag ttg 728
Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu Gln Tyr Ala Gln Leu
135 140 145

MBI15 Sequence Listing.ST25

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ctt acg agt aac aat gag gtt gat tta tca tac tac acg tcg act ctc      776
Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr Tyr Thr Ser Thr Leu
150                               155                               160                               165

ttc agt caa cct ttt tca acg cct tct tca tct tct tct tcc tcc caa      824
Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser Ser Ser Ser Ser Gln
170                               175                               180

cag acg cag caa cag cag cta caa caa caa caa cag cag cgt gaa gaa      872
Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Arg Glu Glu
185                               190                               195

gaa gag aag aat tat ggt tac aat tat tat aac tac cca aga gaa taa      920
Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn Tyr Pro Arg Glu
200                               205                               210

tctaattatt attggtgggc gaatcagttt tataaatagc tatcatagtt tcatttttgg      980

tttccgtaac ctttggtgca tggaaaatat gaatgaacga gggacatgtg taacaatttg      1040

tttgtgtttc gtaaattgta gttgtatttg gatttgctga agtttgattt tctgagcata      1100

aatcatttga cggtcacaaaa aaaaaa                                     1126

```

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<210> 26
<211> 212
<212> PRT
<213> Arabidopsis thaliana

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<400> 26

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Met Val Ser Ala Leu Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro
1                               5                               10                               15

```

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Val Lys Gln Glu Leu Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp
20                               25                               30

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```

Gln Pro Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly
35                               40                               45

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```

Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp
50                               55                               60

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```

Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg
65                               70                               75                               80

```

```

Ala Ala Leu Lys Phe Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu
85                               90                               95

```

```

Arg Val Gln Gly Pro Thr Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg
100                              105                              110

```

```

Gly Val Ser Glu Ser Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro
115                              120                              125

```

```

Ser Thr Thr Thr Thr Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu
130                              135                              140

```

```

Gln Tyr Ala Gln Leu Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr
145                              150                              155                              160

```

```

Tyr Thr Ser Thr Leu Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser
165                              170                              175

```

MBI15 Sequence Listing.ST25

Ser Ser Ser Ser Gln Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln
180 185 190

Gln Gln Arg Glu Glu Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn
195 200 205

Tyr Pro Arg Glu
210

<210> 27
<211> 1152
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (76)..(1008)
<223> G881

<400> 27
gtgaccgaag aaagcaaatt gagactacgc accaactagt cctttgggttt gtatcttaag 60
ataaagggttt cttttt atg gac ggt tct tcg ttt ctc gac atc tct ctc gat 111
Met Asp Gly Ser Ser Phe Leu Asp Ile Ser Leu Asp
1 5 10
ctc aac acc aat cct ttc tcc gca aaa ctt ccg aag aag gag gtc tca 159
Leu Asn Thr Asn Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser
15 20 25
gtt ttg gct tct act cac tta aag agg aaa tgg ttg gag caa gac gag 207
Val Leu Ala Ser Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu
30 35 40
agc gca agt gag tta cga gag gag cta aac aga gtt aat tca gag aac 255
Ser Ala Ser Glu Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn
45 50 55 60
aag aag cta aca gag atg tta gct aga gtc tgt gag agc tac aac gaa 303
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu
65 70 75
cta cat aat cat ttg gag aag ctt cag agt cgc cag agc cct gaa atc 351
Leu His Asn His Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile
80 85 90
gag cag acc gat ata ccg ata aag aaa aga aaa caa gac ccg gat gag 399
Glu Gln Thr Asp Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu
95 100 105
ttc tta ggc ttt cct att gga ctc agt agt gga aaa act gag aac agc 447
Phe Leu Gly Phe Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser
110 115 120
tcc agc aac gaa gat cat cat cat cat cat cag caa cat gag cag aaa 495
Ser Ser Asn Glu Asp His His His His His Gln Gln His Glu Gln Lys
125 130 135 140
aat cag ctt ctt tca tgt aaa aga cca gtc act gat agc ttc aac aaa 543
Asn Gln Leu Leu Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys
145 150 155
gca aaa gtt tcg act gtc tac gtg cct act gaa aca tcg gac aca agc 591
Ala Lys Val Ser Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser
160 165 170
ttg aca gtt aaa gat gga ttt caa tgg agg aaa tac gga caa aag gtt 639
Leu Thr Val Lys Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val
175 180 185

MBI15 Sequence Listing.ST25

```

aca aga gac aac ccg tca cct aga gct tac ttt aga tgc tcg ttt gca      687
Thr Arg Asp Asn Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala
190                               195                               200

ccg tct tgt cca gta aaa aag aag gta caa cgc agc gca gag gat cca      735
Pro Ser Cys Pro Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro
205                               210                               215                               220

tct tta ctt gta gcg aca tac gaa ggg acg cat aac cac ttg ggt cca      783
Ser Leu Leu Val Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro
225                               230                               235

aat gct tct gaa ggg gat gct aca agc cag ggt ggg tca agc aca gtg      831
Asn Ala Ser Glu Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val
240                               245                               250

act ttg gat ctg gtt aat ggc tgt cat aga cta gcg ttg gag aaa aac      879
Thr Leu Asp Leu Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn
255                               260                               265

gaa agg gat aat acg atg caa gag gtt ctg att caa caa atg gcg tca      927
Glu Arg Asp Asn Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser
270                               275                               280

tcg tta aca aaa gat tcg aaa ttt aca gct gct ctt gct gct gct ata      975
Ser Leu Thr Lys Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile
285                               290                               295                               300

tct ggg agg tta atg gag caa tct aga aca tga acgttttttag tgaatgtatt 1028
Ser Gly Arg Leu Met Glu Gln Ser Arg Thr
305                               310

gtttttgttt gtttagaatg attcttcgtt ttogaattgt gtcttttcgat taggagataa 1088
aagatgtata taaatattat aagtagatga agaaatcgta taagtaaaaa aaaaaaaaaa 1148
aaaa                                                    1152

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```

<210> 28
<211> 310
<212> PRT
<213> Arabidopsis thaliana

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```

<400> 28

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Met Asp Gly Ser Ser Phe Leu Asp Ile Ser Leu Asp Leu Asn Thr Asn
1          5          10          15

```

```

Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser Val Leu Ala Ser
20          25          30

```

```

Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu Ser Ala Ser Glu
35          40          45

```

```

Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn Lys Lys Leu Thr
50          55          60

```

```

Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu Leu His Asn His
65          70          75          80

```

```

Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile Glu Gln Thr Asp
85          90          95

```

```

Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu Phe Leu Gly Phe
100         105         110

```

MBI15 Sequence Listing.ST25

Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser Ser Ser Asn Glu
 115 120 125

Asp His His His His His Gln Gln His Glu Gln Lys Asn Gln Leu Leu
 130 135 140

Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys Ala Lys Val Ser
 145 150 155 160

Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser Leu Thr Val Lys
 165 170 175

Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp Asn
 180 185 190

Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala Pro Ser Cys Pro
 195 200 205

Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro Ser Leu Leu Val
 210 215 220

Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro Asn Ala Ser Glu
 225 230 235 240

Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val Thr Leu Asp Leu
 245 250 255

Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn Glu Arg Asp Asn
 260 265 270

Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser Ser Leu Thr Lys
 275 280 285

Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile Ser Gly Arg Leu
 290 295 300

Met Glu Gln Ser Arg Thr
 305 310

<210> 29
 <211> 1276
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (47)..(1150)
 <223> G896

<400> 29
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 Met Tyr Pro
 1

cca cct ccc tca agc atc tac gct cct ccg atg ctg gtg aat tgc tcc 103
 Pro Pro Pro Ser Ser Ile Tyr Ala Pro Pro Met Leu Val Asn Cys Ser
 5 10 15

ggc tgc cgg acg cct ctc cag ctc cca tcc ggc gcc cga tct att cgc 151
 Gly Cys Arg Thr Pro Leu Gln Leu Pro Ser Gly Ala Arg Ser Ile Arg
 20 25 30 35

MBI15 Sequence Listing.ST25

tgc gct ctc tgc cag gct gtt act cat atc gcc gac cct cgc acc gcc Cys Ala Leu Cys Gln Ala Val Thr His Ile Ala Asp Pro Arg Thr Ala 40 45 50	199
cct cct ccg caa cct tcc tcc gcc cct tct ccg cct ccc caa atc cac Pro Pro Pro Gln Pro Ser Ser Ala Pro Ser Pro Pro Pro Gln Ile His 55 60 65	247
gcg cct ccc ggt cag ctg cct cac ccc cat ggc agg aag agg gcc gtg Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys Arg Ala Val 70 75 80	295
atc tgt ggc atc tcg tat cgt ttc tct cgc cac gag ctc aaa ggc tgc Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu Lys Gly Cys 85 90 95	343
atc aac gac gcc aag tgc atg cgt cac ctt ctc atc aac aaa ttc aaa Ile Asn Asp Ala Lys Cys Met Arg His Leu Leu Ile Asn Lys Phe Lys 100 105 110 115	391
ttc tcc cca gat tca att ctc atg ctt acc gag gaa gaa act gat cca Phe Ser Pro Asp Ser Ile Leu Met Leu Thr Glu Glu Glu Thr Asp Pro 120 125 130	439
tat cgt atc ccg acc aag caa aac atg agg atg gca ttg tat tgg ctc Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu Tyr Trp Leu 135 140 145	487
gta cag gga tgc aca gca ggc gac tca ctt gtc ttc cac tac tct ggt Val Gln Gly Cys Thr Ala Gly Asp Ser Leu Val Phe His Tyr Ser Gly 150 155 160	535
cat ggt tcg cgt caa aga aac tac aac ggt gat gaa gtt gat ggc tat His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val Asp Gly Tyr 165 170 175	583
gat gaa aca ctc tgt cct ctg gat ttt gaa act cag ggg atg att gta Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly Met Ile Val 180 185 190 195	631
gac gat gag atc aac gca acc att gta cgc cct ctt cca cat ggt gtc Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro His Gly Val 200 205 210	679
aag ctc cat tca att atc gat gct tgc cat agt ggt acc gtt ctg gat Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr Val Leu Asp 215 220 225	727
tta ccc ttc cta tgc aga atg aac aga gct ggg cag tat gtg tgg gag Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr Val Trp Glu 230 235 240	775
gat cat cgg cct agg tca ggt ttg tgg aaa gga act gct ggt gga gaa Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala Gly Gly Glu 245 250 255	823
gcc att tca att agt gga tgt gat gat gat cag act tcg gcc gac aca Ala Ile Ser Ile Ser Gly Cys Asp Asp Asp Gln Thr Ser Ala Asp Thr 260 265 270 275	871
tca gcg ctg tcg aag atc acg tct acg ggt gct atg act ttc tgt ttt Ser Ala Leu Ser Lys Ile Thr Ser Thr Gly Ala Met Thr Phe Cys Phe 280 285 290	919
att caa gca att gaa cgc agc gca caa ggc aca acc tat gga agc ctt Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr Gly Ser Leu 295 300 305	967
ctg aat tct atg cgc acc aca ata agg aat aca ggg aat gat ggt ggt Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn Asp Gly Gly 310 315 320	1015
ggt agt ggt gga gtt gtg acg act gtg ctg agc atg ctt ctg aca ggg Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu Leu Thr Gly 330 335 340	1063

325

330

335

caa aca ttc gat gtc tat gca aag cct ttc act ctc tag taaaggacaa 1160
Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu
360 365

tcttattttt atttttcttt caaaagaata aaggaaaaca ttgatttggt gattcgt 1276

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<210> 30
<211> 367
<212> PRT
<213> Arabidopsis thaliana
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<400> 30

Met Tyr Pro Pro Pro Pro Ser Ser Ile Tyr Ala Pro Pro Met Leu Val
1 5 10 15

Asn Cys Ser Gly Cys Arg Thr Pro Leu Gln Leu Pro Ser Gly Ala Arg
20 25 30

Ser Ile Arg Cys Ala Leu Cys Gln Ala Val Thr His Ile Ala Asp Pro
35 40 45

Arg Thr Ala Pro Pro Pro Gln Pro Ser Ser Ala Pro Ser Pro Pro Pro
50 55 60

Gln Ile His Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys
65 70 75 80

Arg Ala Val Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu
85 90 95

Lys Gly Cys Ile Asn Asp Ala Lys Cys Met Arg His Leu Leu Ile Asn
100 105 110

Lys Phe Lys Phe Ser Pro Asp Ser Ile Leu Met Leu Thr Glu Glu Glu
115 120 125

Thr Asp Pro Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu
130 135 140

Tyr Trp Leu Val Gln Gly Cys Thr Ala Gly Asp Ser Leu Val Phe His
145 150 155 160

Tyr Ser Gly His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val
165 170 175

Asp Gly Tyr Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly
180 185 190

Met Ile Val Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro
195 200 205

His Gly Val Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr

MBI15 Sequence Listing.ST25

210 215 220

Val Leu Asp Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr
225 230 235 240

Val Trp Glu Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala
245 250 255

Gly Gly Glu Ala Ile Ser Ile Ser Gly Cys Asp Asp Asp Gln Thr Ser
260 265 270

Ala Asp Thr Ser Ala Leu Ser Lys Ile Thr Ser Thr Gly Ala Met Thr
275 280 285

Phe Cys Phe Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr
290 295 300

Gly Ser Leu Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn
305 310 315 320

Asp Gly Gly Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu
325 330 335

Leu Thr Gly Gly Ser Ala Ile Gly Gly Leu Arg Gln Glu Pro Gln Leu
340 345 350

Thr Ala Cys Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu
355 360 365

<210> 31
<211> 726
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(726)
<223> G378

<400> 31 48
atg gcc tcg tca tca tca tca tct tat aga ttc caa tct ggg tct tac
Met Ala Ser Ser Ser Ser Ser Tyr Arg Phe Gln Ser Gly Ser Tyr
1 5 10 15

cct ctt tcg tca agt cct tct ctt ggg aat ttc gtc gaa cgc att aaa 96
Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys
20 25 30

gac gct tgt cat ttc ctt gtc tct gct gtt ttg ggt acc att atc tcc 144
Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser
35 40 45

gcg atc ttg acc ttc ttc ttc gca cta gtg ggc aca ttg cta ggg gca 192
Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala
50 55 60

ctt aca gga gct ttg ata ggt caa gaa act gag agt ggt ttc att aga 240
Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg
65 70 75 80

gga gca gca att gga gcc att tcg gga gct gtt ttc tct atc gag gtc 288
Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val
85 90 95

MBI15 Sequence Listing.ST25

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ttt gaa tca tct ctg gat ctc tgg aaa tcc gat gag tcg ggt ttc gga    336
Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly
      100      105      110

tgt ttt ctc tac ttg att gat gtc att gtt agt ctt cta agc ggg aga    384
Cys Phe Leu Tyr Leu Ile Asp Val Ile Val Ser Leu Leu Ser Gly Arg
      115      120      125

ctt gta cga gag cgc att ggt cct gca atg cta agt gca gtg caa agt    432
Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser
      130      135      140

caa atg gga gct gtg gat aca gct ttt gat gat cac aca agc ctt ttt    480
Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe
      145      150      155

gat aca gga ggc tca aaa gga ttg aca gga gac ctt gtt gag aaa atc    528
Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile
      165      170      175

cca aag atg aca atc act ggc aac aat aac act gat gct tct gag aac    576
Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn
      180      185      190

aca gac tca tgt tct gtt tgt ctt cag gat ttc cag ctc ggt gaa aca    624
Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr
      195      200      205

gtt aga agc ttg cct cat tgt cat cac atg ttt cac tta cct tgc ata    672
Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile
      210      215      220

gac aat tgg ctc ctt aga cac ggt tct tgc ccg atg tgt aga cgt gat    720
Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp
      225      230      235      240

att taa    726
Ile

```

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<210> 32
<211> 241
<212> PRT
<213> Arabidopsis thaliana

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<400> 32

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Met Ala Ser Ser Ser Ser Ser Tyr Arg Phe Gln Ser Gly Ser Tyr
1      5      10      15

Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys
20     25     30

Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser
35     40     45

Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala
50     55     60

Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg
65     70     75     80

Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val
85     90     95

Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly
100    105    110

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MBI15 Sequence Listing.ST25

Cys Phe Leu Tyr Leu Ile Asp Val Ile Val Ser Leu Leu Ser Gly Arg
 115 120 125
 Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser
 130 135 140
 Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe
 145 150 155 160
 Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile
 165 170 175
 Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn
 180 185 190
 Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr
 195 200 205
 Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile
 210 215 220
 Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp
 225 230 235 240

Ile

<210> 33
 <211> 1370
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (184)..(969)
 <223> G569

<400> 33
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 agactataaaa gggtttttga ttgattcggg agctcgagat ttgacttctt ttagctgatt 120
 cggcaagttt gtatctagaa aggatcgatt ggtgagggtca atagtgggtg gtgggtttta 180
 gta atg gaa gac ggt gag ctt gat ttc tcc aat cag gaa gtg ttt tcg 228
 Met Glu Asp Gly Glu Leu Asp Phe Ser Asn Gln Glu Val Phe Ser 15
 1 5 10
 agt tcg gag atg ggt gaa tta cca cct agc aat tgt tcg atg gat agt 276
 Ser Ser Glu Met Gly Glu Leu Pro Pro Ser Asn Cys Ser Met Asp Ser 20 25 30
 ttc ttt gat ggg ctt tta atg gat act aat gct gct tgt acc cac act 324
 Phe Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr 35 40 45
 cac acc tgt aac ccc act gga cca gag aac act cat act cac acg tgc 372
 His Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys 50 55 60
 ttc cat gtc cac acc aag att ctc ccg gat gag agc gat gaa aaa gtt 420
 Phe His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val 65 70 75

MBI15 Sequence Listing.ST25

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tct act gat gat aca gct gag tct tgt ggg aag aag ggt gaa aag aga 468
Ser Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg
80 85 90 95

cct ttg gga aac cgg gaa gcg gtt aga aag tat aga gag aag aag aag 516
Pro Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys
100 105 110

gct aaa gct gct tct ttg gag gat gag gtt gca agg ctt agg gcg gtg 564
Ala Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val
115 120 125

aat cag cag ctg gtg aag agg ttg caa aat cag gct acc ttg gaa gct 612
Asn Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala
130 135 140

gag gtt tcg agg ctt aag tgt ttg ctt gtg gat ttg aga gga aga ata 660
Glu Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile
145 150 155

gat gga gag att gga tct ttt cct tat cag aaa cct atg gct gca aat 708
Asp Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn
160 165 170 175

att cct tct ttc tcg cac atg atg aat cct tgt aat gta caa tgt gat 756
Ile Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp
180 185 190

gat gaa gtt tat tgc cct cag aat gtg ttt gga gtg aat agc caa gaa 804
Asp Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu
195 200 205

ggg gcc tcg atc aat gac caa ggg tta agt ggt tgt gat ttt gat cag 852
Gly Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln
210 215 220

cta caa tgc atg gct aat cag aac tta aat gga aat gga aac gga tca 900
Leu Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser
225 230 235

ttc agc aac gtc aat aca tct gtc tcg aat aag aga aaa ggt ggg cat 948
Phe Ser Asn Val Asn Thr Ser Val Ser Asn Lys Arg Lys Gly Gly His
240 245 250 255

cgt gca tca aga gca gtt tga agcatcatca agcttggtact atctatttcc 999
Arg Ala Ser Arg Ala Val
260

accagcatag atattgtatt ccaaataagt ttagaggttc agctgcagga tcagcttcgc 1059

tcagcttttga ggggttggtg gtgtggtctt tctttgtggc acgagtgaga tctatggaca 1119

gaaccagat ttagtagtag tagaggcagg atttcgactt ccactaacca tcatgttgct 1179

tggtgaagaa caaggtatgc ccatgaagca cactgttttg tacattgagc ttgaggggct 1239

gtctctgata tagccttact gtaacattgc aacgtttctca caattgtgat cccaagttgc 1299

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aaaaaaaaa a 1370

<210> 34
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<212> PRT
<213> Arabidopsis thaliana

<400> 34

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Ser Glu Met Gly Glu Leu Pro Pro Ser Asn Cys Ser Met Asp Ser Phe

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MBI15 Sequence Listing.ST25

20

25

30

Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr His
 35 40 45

Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys Phe
 50 55 60

His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val Ser
 65 70 75 80

Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg Pro
 85 90 95

Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys Ala
 100 105 110

Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val Asn
 115 120 125

Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala Glu
 130 135 140

Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile Asp
 145 150 155 160

Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn Ile
 165 170 175

Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp Asp
 180 185 190

Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu Gly
 195 200 205

Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln Leu
 210 215 220

Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser Phe
 225 230 235 240

Ser Asn Val Asn Thr Ser Val Ser Asn Lys Arg Lys Gly Gly His Arg
 245 250 255

Ala Ser Arg Ala Val
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MBI15 Sequence Listing.ST25

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acatttggtc ctgattcatt tcctattggt tcgtattgtc tgtgcacaca agagaaattt	180
caagaagttg ttactaaaag agaggccaca agtggatatt gtctttgtta tcaagtgtta	240
gtacagaaaa gtggtgagaa agtaat atg gct gat acc agt ccg aga act gat	293
Met Ala Asp Thr Ser Pro Arg Thr Asp	
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gtc tca aca gat gac gac aca gat cat cct gat ctt ggg tcg gag gga	341
Val Ser Thr Asp Asp Asp Thr Asp His Pro Asp Leu Gly Ser Glu Gly	
10 15 20 25	
gca cta gtg aat act gct gct tct gat tcg agt gac cga tcg aag gga	389
Ala Leu Val Asn Thr Ala Ala Ser Asp Ser Ser Asp Arg Ser Lys Gly	
30 35 40	
aag atg gat caa aag act ctt cgt agg ctt gct caa aac cgt gag gca	437
Lys Met Asp Gln Lys Thr Leu Arg Arg Leu Ala Gln Asn Arg Glu Ala	
45 50 55	
gca agg aaa agc aga ttg agg aag aag gct tat gtt cag cag cta gag	485
Ala Arg Lys Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu	
60 65 70	
aac agc cgc ttg aaa cta acc cag ctt gag cag gag ctg caa aga gca	533
Asn Ser Arg Leu Lys Leu Thr Gln Leu Glu Gln Glu Leu Gln Arg Ala	
75 80 85	
aga cag cag ggc gtc ttc att tca ggc aca gga gac cag gcc cat tct	581
Arg Gln Gln Gly Val Phe Ile Ser Gly Thr Gly Asp Gln Ala His Ser	
90 95 100 105	
act ggt gga aat ggt gct ttg gcg ttt gat gct gaa cat tca cgg tgg	629
Thr Gly Gly Asn Gly Ala Leu Ala Phe Asp Ala Glu His Ser Arg Trp	
110 115 120	
ttg gaa gaa aag aac aag caa atg aac gag ctg agg tct gct ctg aat	677
Leu Glu Glu Lys Asn Lys Gln Met Asn Glu Leu Arg Ser Ala Leu Asn	
125 130 135	
gcg cat gca ggt gat tct gag ctt cga ata ata gtc gat ggt gtg atg	725
Ala His Ala Gly Asp Ser Glu Leu Arg Ile Ile Val Asp Gly Val Met	
140 145 150	
gct cac tat gag gag ctt ttc agg ata aag agc aat gca gct aag aat	773
Ala His Tyr Glu Glu Leu Phe Arg Ile Lys Ser Asn Ala Ala Lys Asn	
155 160 165	
gat gtc ttt cac ttg cta tct ggc atg tgg aaa aca cca gct gag aga	821
Asp Val Phe His Leu Leu Ser Gly Met Trp Lys Thr Pro Ala Glu Arg	
170 175 180 185	
tgt ttc ttg tgg ctc ggt gga ttt cgt tca tcc gaa ctt cta aag ctt	869
Cys Phe Leu Trp Leu Gly Gly Phe Arg Ser Ser Glu Leu Leu Lys Leu	
190 195 200	
ctg gcg aat cag ttg gag cca atg aca gag aga cag ttg atg ggc ata	917
Leu Ala Asn Gln Leu Glu Pro Met Thr Glu Arg Gln Leu Met Gly Ile	
205 210 215	
aat aac ctg caa cag aca tcg cag cag gct gaa gat gct ttg tct caa	965
Asn Asn Leu Gln Gln Thr Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln	
220 225 230	
ggg atg gag agc tta caa cag tca cta gct gat act tta tcg agc ggg	1013
Gly Met Glu Ser Leu Gln Gln Ser Leu Ala Asp Thr Leu Ser Ser Gly	
235 240 245	
act ctt ggt tca agt tca tca ggg aat gtc gca agc tac atg ggt cag	1061
Thr Leu Gly Ser Ser Ser Ser Gly Asn Val Ala Ser Tyr Met Gly Gln	
250 255 260 265	

MBI15 Sequence Listing.ST25

atg gcc atg gca atg gga aag tta ggt aca ctc gaa gga ttt atc cgc 1109
 Met Ala Met Ala Met Gly Lys Leu Gly Thr Leu Glu Gly Phe Ile Arg
 270 275 280

cag gct gat aat ttg aga cta caa aca ttg caa cag atg ata aga gta 1157
 Gln Ala Asp Asn Leu Arg Leu Gln Thr Leu Gln Gln Met Ile Arg Val
 285 290 295

tta aca acg aga cag tca gca cgt gct cta ctt gca ata cac gat tac 1205
 Leu Thr Thr Arg Gln Ser Ala Arg Ala Leu Leu Ala Ile His Asp Tyr
 300 305 310

ttc tca cgg cta cga gct cta agc tcc tta tgg ctt gct cga ccc aga 1253
 Phe Ser Arg Leu Arg Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg
 315 320 325

gag tga aactgtatctt tgggtcacatg tcagctgtac aaaatccata tggacacaaa 1309
 Glu
 330

accaggagag actattaatc aacacttgct agattcttct taccaaattcc atcaacaaat 1369

aagcaaattt ctgggaaaca aaagactctt tgtatgtagg tttcttctac atggttgtgg 1429

taattcatgt tgttttagtt gtagtcatca gtttttaatt tagcatttga aaagttcaat 1489

gttgtttata tagcatcttc gattatctta gaaagggtat tgaattttgt ttttttttgt 1549

tacttttgtg tgtggttaaag gtgttttaac cttgcaactt ctgtactgta atcatttaac 1609

aatattaaga tgttctatctt gagttttgt 1638

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 <213> Arabidopsis thaliana

<400> 36

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Asp His Pro Asp Leu Gly Ser Glu Gly Ala Leu Val Asn Thr Ala Ala
 20 25 30

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 35 40 45

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
 50 55 60

Lys Lys Ala Tyr Val Gln Gln Leu Glu Asn Ser Arg Leu Lys Leu Thr
 65 70 75 80

Gln Leu Glu Gln Glu Leu Gln Arg Ala Arg Gln Gln Gly Val Phe Ile
 85 90 95

Ser Gly Thr Gly Asp Gln Ala His Ser Thr Gly Gly Asn Gly Ala Leu
 100 105 110

Ala Phe Asp Ala Glu His Ser Arg Trp Leu Glu Glu Lys Asn Lys Gln
 115 120 125

Met Asn Glu Leu Arg Ser Ala Leu Asn Ala His Ala Gly Asp Ser Glu
 130 135 140

MBI15 Sequence Listing.ST25

Leu Arg Ile Ile Val Asp Gly Val Met Ala His Tyr Glu Glu Leu Phe
145 150 155 160

Arg Ile Lys Ser Asn Ala Ala Lys Asn Asp Val Phe His Leu Leu Ser
165 170 175

Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu Trp Leu Gly Gly
180 185 190

Phe Arg Ser Ser Glu Leu Leu Lys Leu Leu Ala Asn Gln Leu Glu Pro
195 200 205

Met Thr Glu Arg Gln Leu Met Gly Ile Asn Asn Leu Gln Gln Thr Ser
210 215 220

Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Glu Ser Leu Gln Gln
225 230 235 240

Ser Leu Ala Asp Thr Leu Ser Ser Gly Thr Leu Gly Ser Ser Ser Ser
245 250 255

Gly Asn Val Ala Ser Tyr Met Gly Gln Met Ala Met Ala Met Gly Lys
260 265 270

Leu Gly Thr Leu Glu Gly Phe Ile Arg Gln Ala Asp Asn Leu Arg Leu
275 280 285

Gln Thr Leu Gln Gln Met Ile Arg Val Leu Thr Thr Arg Gln Ser Ala
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Arg Ala Leu Leu Ala Ile His Asp Tyr Phe Ser Arg Leu Arg Ala Leu
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Met Asp Gly Glu Asp Phe Ala Gly Lys Ala
1 5 10

gct gct gaa gcc aag gga ttg aac ccg gga tta atc gtg ctg ctt gtt 160
Ala Ala Glu Ala Lys Gly Leu Asn Pro Gly Leu Ile Val Leu Leu Val
15 20 25

gtt gga ggt ccg ctt ctt gtg ttc cta atc gcc aac tac gtg ctt tac 208
Val Gly Gly Pro Leu Leu Val Phe Leu Ile Ala Asn Tyr Val Leu Tyr
30 35 40

MBI15 Sequence Listing.ST25

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Val Tyr Ala Gln Lys Asn Leu Pro Pro Arg Lys Lys Lys Pro Val Ser
45 50 55

aaa aag aag ctc aag cgg gag aag cta aag caa gga gtc cct gtc cct 304
Lys Lys Lys Leu Lys Arg Glu Lys Leu Lys Gln Gly Val Pro Val Pro
60 65 70

gga gaa taa aagccagctt aagcttcctt cacttggtgcc tccttcaaag 353
Gly Glu
75

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catgaggatt atctttgagg cct 436

<210> 38
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<212> PRT
<213> Arabidopsis thaliana

<400> 38

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20 25 30

Val Phe Leu Ile Ala Asn Tyr Val Leu Tyr Val Tyr Ala Gln Lys Asn
35 40 45

Leu Pro Pro Arg Lys Lys Lys Pro Val Ser Lys Lys Lys Leu Lys Arg
50 55 60

Glu Lys Leu Lys Gln Gly Val Pro Val Pro Gly Glu
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<222> (280)..(1317)
<223> G265

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aatcaaaga gacttttgaa gattgtttcc caatttgctt caatcgggat cgagtcaaag 180

ctgaaatctt ctccactcat catctgacta taagacttaa tcaagggact ttttggtcgg 240

gtttggtttt aaacgtcttg gattcgaagt gggttaaggt atg gat gaa aat aat 294
Met Asp Glu Asn Asn
1 5

gga ggt tca agc tca ctt cca cct ttc ctt act aaa aca tat gaa atg 342
Gly Gly Ser Ser Ser Leu Pro Pro Phe Leu Thr Lys Thr Tyr Glu Met
10 15 20

ggt gat gat tct tct tct gac tcg gtc gtt gct tgg agc gaa aac aac 390
Val Asp Asp Ser Ser Ser Asp Ser Val Val Ala Trp Ser Glu Asn Asn

MBI15 Sequence Listing.ST25

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ccg aga ttc ttc aag cat aag aat ttc tca agt ttc atc cgt cag ctt Pro Arg Phe Phe Lys His Lys Asn Phe Ser Ser Phe Ile Arg Gln Leu 55 60 65			486
aat aca tat ggt ttt cga aaa gta gat cct gag aaa tgg gaa ttc ttg Asn Thr Tyr Gly Phe Arg Lys Val Asp Pro Glu Lys Trp Glu Phe Leu 70 75 80 85			534
aat gat gat ttt gtt aga ggt cga cct tac ctt atg aag aac att cat Asn Asp Asp Phe Val Arg Gly Arg Pro Tyr Leu Met Lys Asn Ile His 90 95 100			582
aga cga aaa ccg gtt cat agc cac tcg tta gtg aat cta caa gcg caa Arg Arg Lys Pro Val His Ser His Ser Leu Val Asn Leu Gln Ala Gln 105 110 115			630
aat cct ttg acg gaa tca gaa aga cgg agc atg gag gat cag ata gaa Asn Pro Leu Thr Glu Ser Glu Arg Arg Ser Met Glu Asp Gln Ile Glu 120 125 130			678
aga ctg aaa aat gag aaa gaa ggc ctt ctt gcg gag tta cag aac caa Arg Leu Lys Asn Glu Lys Glu Gly Leu Leu Ala Glu Leu Gln Asn Gln 135 140 145			726
gag caa gaa cgg aaa gag ttt gag ctg caa gta acg aca ttg aaa gat Glu Gln Glu Arg Lys Glu Phe Glu Leu Gln Val Thr Thr Leu Lys Asp 150 155 160 165			774
cgg tta caa cat atg gaa caa cat cag aaa tca ata gtg gca tat gtt Arg Leu Gln His Met Glu Gln His Gln Lys Ser Ile Val Ala Tyr Val 170 175 180			822
tca cag gtt ttg gga aaa cca gga ctt tca cta aac ctc gaa aac cat Ser Gln Val Leu Gly Lys Pro Gly Leu Ser Leu Asn Leu Glu Asn His 185 190 195			870
gag aga aga aaa aga aga ttt caa gag aac tct ctt cct cca agc agt Glu Arg Arg Lys Arg Arg Phe Gln Glu Asn Ser Leu Pro Pro Ser Ser 200 205 210			918
tca cac ata gaa cag gtc gaa aag tta gaa tct tcg cta acg ttt tgg Ser His Ile Glu Gln Val Glu Lys Leu Glu Ser Ser Leu Thr Phe Trp 215 220 225			966
gag aat ctt gta tcg gaa tca tgc gag aag agc ggt ttg cag tca tca Glu Asn Leu Val Ser Glu Ser Cys Glu Lys Ser Gly Leu Gln Ser Ser 230 235 240 245			1014
agc atg gat cat gat gca gct gag tca agt cta agt att ggc gat aca Ser Met Asp His Asp Ala Ala Glu Ser Ser Leu Ser Ile Gly Asp Thr 250 255 260			1062
cga ccc aaa tca tcg aag att gat atg aac tca gag ccg ccc gtt acc Arg Pro Lys Ser Ser Lys Ile Asp Met Asn Ser Glu Pro Pro Val Thr 265 270 275			1110
gtt act gcg cct gct cca aaa aca ggc gtt aac gat gac ttt tgg gaa Val Thr Ala Pro Ala Pro Lys Thr Gly Val Asn Asp Asp Phe Trp Glu 280 285 290			1158
caa tgt ttg aca gag aac cct gga tca acc gag caa caa gaa gtt cag Gln Cys Leu Thr Glu Asn Pro Gly Ser Thr Glu Gln Gln Glu Val Gln 295 300 305			1206
tca gag aga aga gat gtc ggt aat gat aat aat ggt aat aag att gga Ser Glu Arg Arg Asp Val Gly Asn Asp Asn Asn Gly Asn Lys Ile Gly 310 315 320 325			1254
aat caa agg acg tat tgg tgg aat tca ggg aat gta aat aac att aca			1302

MBI15 Sequence Listing.ST25

Asn Gln Arg Thr Tyr Trp Trp Asn Ser Gly Asn Val Asn Asn Ile Thr
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 Glu Lys Ala Ser
 345
 actgagatta ttgtatgtgt tcattattta ttactctggt tctgtaaaaa caaatctctc 1417
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 <211> 345
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 40
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 Trp Ser Glu Asn Asn Lys Ser Phe Ile Val Lys Asn Pro Ala Glu Phe
 35 40 45
 Ser Arg Asp Leu Leu Pro Arg Phe Phe Lys His Lys Asn Phe Ser Ser
 50 55 60
 Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Val Asp Pro Glu
 65 70 75 80
 Lys Trp Glu Phe Leu Asn Asp Asp Phe Val Arg Gly Arg Pro Tyr Leu
 85 90 95
 Met Lys Asn Ile His Arg Arg Lys Pro Val His Ser His Ser Leu Val
 100 105 110
 Asn Leu Gln Ala Gln Asn Pro Leu Thr Glu Ser Glu Arg Arg Ser Met
 115 120 125
 Glu Asp Gln Ile Glu Arg Leu Lys Asn Glu Lys Glu Gly Leu Leu Ala
 130 135 140
 Glu Leu Gln Asn Gln Glu Gln Glu Arg Lys Glu Phe Glu Leu Gln Val
 145 150 155 160
 Thr Thr Leu Lys Asp Arg Leu Gln His Met Glu Gln His Gln Lys Ser
 165 170 175
 Ile Val Ala Tyr Val Ser Gln Val Leu Gly Lys Pro Gly Leu Ser Leu
 180 185 190
 Asn Leu Glu Asn His Glu Arg Arg Lys Arg Arg Phe Gln Glu Asn Ser
 195 200 205
 Leu Pro Pro Ser Ser Ser His Ile Glu Gln Val Glu Lys Leu Glu Ser
 210 215 220

MBI15 Sequence Listing.ST25

Ser Leu Thr Phe Trp Glu Asn Leu Val Ser Glu Ser Cys Glu Lys Ser
225 230 235 240

Gly Leu Gln Ser Ser Ser Met Asp His Asp Ala Ala Glu Ser Ser Leu
245 250 255

Ser Ile Gly Asp Thr Arg Pro Lys Ser Ser Lys Ile Asp Met Asn Ser
260 265 270

Glu Pro Pro Val Thr Val Thr Ala Pro Ala Pro Lys Thr Gly Val Asn
275 280 285

Asp Asp Phe Trp Glu Gln Cys Leu Thr Glu Asn Pro Gly Ser Thr Glu
290 295 300

Gln Gln Glu Val Gln Ser Glu Arg Arg Asp Val Gly Asn Asp Asn Asn
305 310 315 320

Gly Asn Lys Ile Gly Asn Gln Arg Thr Tyr Trp Trp Asn Ser Gly Asn
325 330 335

Val Asn Asn Ile Thr Glu Lys Ala Ser
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<210> 41
<211> 913
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<222> (52)..(783)
<223> G1006

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Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser Ile Thr
5 10 15

cgt cac ttg cta gga gga gga gga gag aac gag ctg cga ctc aat gag 153
Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu Asn Glu
20 25 30

tca aca ccg agt tcg tgt ttc aca gag agt tgg gga ggt ttg cca ttg 201
Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu Pro Leu
35 40 45 50

aaa gag aat gat tca gag gac atg ttg gtg tac gga ctc ctc aaa gat 249
Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu Lys Asp
55 60 65

gcc ttc cat ttt gac acg tca tca tcg gac ttg agc tgt ctt ttt gat 297
Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu Phe Asp
70 75 80

ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg atg gag 345
Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala Met Glu
85 90 95

gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg aag gcg 393
Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val Lys Ala
100 105 110

MBI15 Sequence Listing.ST25

aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc gcg gcg 441
 Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala
 115 120 125 130

gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta ggg acg 489
 Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr
 135 140 145

ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct gct ttt 537
 Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala Ala Phe
 150 155 160

agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg gtt aat 585
 Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val Asn
 165 170 175

tcc ggt gaa cct gac ccg gtt cgg atc acg tct aag aga tct tct tcg 633
 Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser Ser Ser
 180 185 190

tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac ggg aag 681
 Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn Gly Lys
 195 200 205 210

ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg gtg cag 729
 Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val Val Gln
 215 220 225

gtg aag tgt gag gtt ggt gat gag aca cgt gtt gat gag tta ttg gtt 777
 Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu Leu Val
 230 235 240

tca taa gtttgatctt gtgtgttttg tagttgaata gttttgctat aaatgttgag 833
 Ser

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aatcaaaaaa aaaaaaaaaa 913

<210> 42
 <211> 243
 <212> PRT
 <213> Arabidopsis thaliana

<400> 42

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Ile Thr Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu
 20 25 30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
 35 40 45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
 50 55 60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu
 65 70 75 80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
 85 90 95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val
 100 105 110

MBI15 Sequence Listing.ST25

Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
 115 120 125

Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
 130 135 140

Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala
 145 150 155 160

Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
 165 170 175

Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser
 180 185 190

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn
 195 200 205

Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val
 210 215 220

Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu
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Leu Val Ser

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 <223> G1309

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aaa tct gga gag aga cca aaa cag aga cag agg aaa ggg tta tgg tca 106
 Lys Ser Gly Glu Arg Pro Lys Gln Arg Gln Arg Lys Gly Leu Trp Ser
 5 10 15

cct gaa gaa gac cag aag ctc aag agt ttc atc ctc tct cgt ggc cat 154
 Pro Glu Glu Asp Gln Lys Leu Lys Ser Phe Ile Leu Ser Arg Gly His
 20 25 30

gct tgc tgg acc act gtt ccc atc cta gct gga ttg caa agg aat ggg 202
 Ala Cys Trp Thr Thr Val Pro Ile Leu Ala Gly Leu Gln Arg Asn Gly
 35 40 45 50

aaa agc tgc aga tta agg tgg att aat tac cta aga cca gga cta aag 250
 Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
 55 60 65

agg ggg tcg ttt agt gaa gaa gaa gaa gag acc atc ttg act tta cat 298
 Arg Gly Ser Phe Ser Glu Glu Glu Glu Glu Thr Ile Leu Thr Leu His
 70 75 80

tct tcc ttg ggt aac aag tgg tct cgg att gca aaa tat tta ccg gga 346

MBI15 Sequence Listing.ST25

Ser Ser Leu Gly Asn Lys Trp Ser Arg Ile Ala Lys Tyr Leu Pro Gly
85 90 95

aga aca gac aac gag att aag aac tat tgg cat tcc tat ctg aag aag 394
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser Tyr Leu Lys Lys
100 105 110

aga tgg ctc aaa tct caa cca caa ctc aaa agc caa ata tca gac ctc 442
Arg Trp Leu Lys Ser Gln Pro Gln Leu Lys Ser Gln Ile Ser Asp Leu
115 120 125 130

aca gaa tct cct tct tca cta ctt tct tgc ggg aaa aga aat ctg gaa 490
Thr Glu Ser Pro Ser Ser Leu Leu Ser Cys Gly Lys Arg Asn Leu Glu
135 140 145

acc gaa acc cta gat cac gtg atc tcc ttc cag aaa ttt tca gag aat 538
Thr Glu Thr Leu Asp His Val Ile Ser Phe Gln Lys Phe Ser Glu Asn
150 155 160

cca act tca tca cca tcc aaa gaa agc aac aac aac atg atc atg aac 586
Pro Thr Ser Ser Pro Ser Lys Glu Ser Asn Asn Asn Met Ile Met Asn
165 170 175

aac agt aat aac ttg cct aaa ctg ttc ttc tct gag tgg atc agt tct 634
Asn Ser Asn Asn Leu Pro Lys Leu Phe Phe Ser Glu Trp Ile Ser Ser
180 185 190

tca aat cca cac atc gat tac tcc tct gct ttt aca gat tcc aag cac 682
Ser Asn Pro His Ile Asp Tyr Ser Ser Ala Phe Thr Asp Ser Lys His
195 200 205 210

att aat gaa act caa gat caa atc aat gaa gag gaa gtg atg atg atc 730
Ile Asn Glu Thr Gln Asp Gln Ile Asn Glu Glu Glu Val Met Met Ile
215 220 225

aat aac aac aac tac tct tca ctt gag gat gtc atg ctc cgt aca gat 778
Asn Asn Asn Asn Tyr Ser Ser Leu Glu Asp Val Met Leu Arg Thr Asp
230 235 240

ttt ttg cag cct gat cat gaa tat gca aat tat tat tct tct gga gat 826
Phe Leu Gln Pro Asp His Glu Tyr Ala Asn Tyr Tyr Ser Ser Gly Asp
245 250 255

ttc ttc atc aac agt gac caa aat tat gtc taa gaagagtga tatgatcgta 879
Phe Phe Ile Asn Ser Asp Gln Asn Tyr Val
260 265

agaggaacat aagctagtta cttgtgttac agc 912

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<212> PRT
<213> Arabidopsis thaliana

<400> 44

Met Thr Lys Ser Gly Glu Arg Pro Lys Gln Arg Gln Arg Lys Gly Leu
1 5 10 15

Trp Ser Pro Glu Glu Asp Gln Lys Leu Lys Ser Phe Ile Leu Ser Arg
20 25 30

Gly His Ala Cys Trp Thr Thr Val Pro Ile Leu Ala Gly Leu Gln Arg
35 40 45

Asn Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly
50 55 60

Leu Lys Arg Gly Ser Phe Ser Glu Glu Glu Glu Thr Ile Leu Thr
65 70 75 80

MBI15 Sequence Listing.ST25

Leu His Ser Ser Leu Gly Asn Lys Trp Ser Arg Ile Ala Lys Tyr Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser Tyr Leu
 100 105 110
 Lys Lys Arg Trp Leu Lys Ser Gln Pro Gln Leu Lys Ser Gln Ile Ser
 115 120 125
 Asp Leu Thr Glu Ser Pro Ser Ser Leu Leu Ser Cys Gly Lys Arg Asn
 130 135 140
 Leu Glu Thr Glu Thr Leu Asp His Val Ile Ser Phe Gln Lys Phe Ser
 145 150 155 160
 Glu Asn Pro Thr Ser Ser Pro Ser Lys Glu Ser Asn Asn Asn Met Ile
 165 170 175
 Met Asn Asn Ser Asn Asn Leu Pro Lys Leu Phe Phe Ser Glu Trp Ile
 180 185 190
 Ser Ser Ser Asn Pro His Ile Asp Tyr Ser Ser Ala Phe Thr Asp Ser
 195 200 205
 Lys His Ile Asn Glu Thr Gln Asp Gln Ile Asn Glu Glu Glu Val Met
 210 215 220
 Met Ile Asn Asn Asn Asn Tyr Ser Ser Leu Glu Asp Val Met Leu Arg
 225 230 235 240
 Thr Asp Phe Leu Gln Pro Asp His Glu Tyr Ala Asn Tyr Tyr Ser Ser
 245 250 255
 Gly Asp Phe Phe Ile Asn Ser Asp Gln Asn Tyr Val
 260 265

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 <212> DNA
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 <222> (1)..(1575)
 <223> G2550

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 Met Ala Val Tyr Tyr Pro Asn Ser Val Gly Met Gln Ser Leu Tyr Gln
 1 5 10 15
 gaa tcc att tac ctc aac gaa caa caa caa caa caa caa gct tct 96
 Glu Ser Ile Tyr Leu Asn Glu Gln Gln Gln Gln Gln Gln Ala Ser
 20 25 30
 tct tcc tct gct gca tct ttc tcc gag att gtt tcc ggt gat gtt cga 144
 Ser Ser Ser Ala Ala Ser Phe Ser Glu Ile Val Ser Gly Asp Val Arg
 35 40 45
 aac aac gag atg gta ttt atc cca cca aca agc gac gta gcc gtc aac 192

MBI15 Sequence Listing.ST25

Asn	Asn	Glu	Met	Val	Phe	Ile	Pro	Pro	Thr	Ser	Asp	Val	Ala	Val	Asn	
50						55					60					
gga	aac	gta	acg	gtg	tca	agt	aac	gat	cta	agc	ttt	cac	ggg	gga	gga	240
Gly	Asn	Val	Thr	Val	Ser	Ser	Asn	Asp	Leu	Ser	Phe	His	Gly	Gly	Gly	
65					70					75					80	
ctt	tct	tta	agt	ctt	ggg	aat	cag	atc	cag	tca	gct	gtc	tct	gtt	tct	288
Leu	Ser	Leu	Ser	Leu	Gly	Asn	Gln	Ile	Gln	Ser	Ala	Val	Ser	Val	Ser	
				85					90					95		
ccg	ttt	cag	tat	cat	tac	cag	aat	ctt	tcg	aac	caa	ttg	agt	tac	aat	336
Pro	Phe	Gln	Tyr	His	Tyr	Gln	Asn	Leu	Ser	Asn	Gln	Leu	Ser	Tyr	Asn	
			100					105					110			
aat	ctt	aat	cct	tct	act	atg	tct	gat	gag	aat	ggg	aag	agc	ttg	agt	384
Asn	Leu	Asn	Pro	Ser	Thr	Met	Ser	Asp	Glu	Asn	Gly	Lys	Ser	Leu	Ser	
		115					120					125				
gtt	cat	cag	cat	cac	tct	gat	caa	att	tta	cct	tcc	tct	gtt	tac	aac	432
Val	His	Gln	His	His	Ser	Asp	Gln	Ile	Leu	Pro	Ser	Ser	Val	Tyr	Asn	
						135					140					
aac	aat	ggg	aat	aat	ggg	gtt	gga	ttc	tac	aac	aat	tac	cgt	tac	gag	480
Asn	Asn	Gly	Asn	Asn	Gly	Val	Gly	Phe	Tyr	Asn	Asn	Tyr	Arg	Tyr	Glu	
145					150					155					160	
aca	tca	ggg	ttt	gtg	agt	agt	gta	ctg	aga	tct	cgt	tac	ctt	aaa	cca	528
Thr	Ser	Gly	Phe	Val	Ser	Ser	Val	Leu	Arg	Ser	Arg	Tyr	Leu	Lys	Pro	
				165					170					175		
aca	caa	caa	ttg	ctt	gat	gaa	gtt	gtt	agt	gta	agg	aaa	gat	ttg	aaa	576
Thr	Gln	Gln	Leu	Leu	Asp	Glu	Val	Val	Ser	Val	Arg	Lys	Asp	Leu	Lys	
			180					185					190			
ttg	ggg	aat	aag	aag	atg	aag	aat	gat	aaa	ggg	caa	gac	ttt	cac	aat	624
Leu	Gly	Asn	Lys	Lys	Met	Lys	Asn	Asp	Lys	Gly	Gln	Asp	Phe	His	Asn	
		195					200					205				
ggg	tct	agt	gat	aac	att	aca	gaa	gat	gat	aaa	tct	caa	tcg	cag	gag	672
Gly	Ser	Ser	Asp	Asn	Ile	Thr	Glu	Asp	Asp	Lys	Ser	Gln	Ser	Gln	Glu	
		210				215					220					
ttg	tct	cct	tca	gaa	cgt	cag	gag	cta	cag	agc	aag	aag	agc	aag	ctt	720
Leu	Ser	Pro	Ser	Glu	Arg	Gln	Glu	Leu	Gln	Ser	Lys	Lys	Ser	Lys	Leu	
225					230					235					240	
tta	aca	atg	gtg	gat	gag	gta	gat	aaa	agg	tat	aac	caa	tac	cat	cat	768
Leu	Thr	Met	Val	Asp	Glu	Val	Asp	Lys	Arg	Tyr	Asn	Gln	Tyr	His	His	
				245					250					255		
caa	atg	gaa	gct	tta	gca	tcg	tct	ttc	gag	atg	gta	aca	ggg	ctt	gga	816
Gln	Met	Glu	Ala	Leu	Ala	Ser	Ser	Phe	Glu	Met	Val	Thr	Gly	Leu	Gly	
			260					265					270			
gca	gct	aag	cct	tac	aca	tcc	gta	gct	ctg	aat	aga	atc	tct	cgc	cat	864
Ala	Ala	Lys	Pro	Tyr	Thr	Ser	Val	Ala	Leu	Asn	Arg	Ile	Ser	Arg	His	
		275					280					285				
ttc	cgc	tgt	tta	cgc	gac	gcg	ata	aaa	gaa	cag	att	cag	gtg	atc	aga	912
Phe	Arg	Cys	Leu	Arg	Asp	Ala	Ile	Lys	Glu	Gln	Ile	Gln	Val	Ile	Arg	
		290				295					300					
ggg	aag	ctt	ggg	gag	aga	gag	act	tct	gat	gaa	caa	gga	gag	agg	ata	960
Gly	Lys	Leu	Gly	Glu	Arg	Glu	Thr	Ser	Asp	Glu	Gln	Gly	Glu	Arg	Ile	
305					310					315					320	
ccg	cgt	ctt	agg	tac	tta	gat	caa	cgg	ttg	aga	caa	cag	aga	gct	ttg	1008
Pro	Arg	Leu	Arg	Tyr	Leu	Asp	Gln	Arg	Leu	Arg	Gln	Gln	Arg	Ala	Leu	
				325					330					335		
cat	caa	caa	ctt	gga	atg	gtt	aga	cca	gct	tgg	aga	cca	caa	aga	ggc	1056
His	Gln	Gln	Leu	Gly	Met	Val	Arg	Pro	Ala	Trp	Arg	Pro	Gln	Arg	Gly	
			340					345					350			

MBI15 Sequence Listing.ST25

tta cct gaa aac tct gtc tct	ata ctt cga gct tgg ctc ttt gag cat	1104
Leu Pro Glu Asn Ser Val Ser	Ile Leu Arg Ala Trp Leu Phe Glu His	
355	360 365	
ttc ctt cat cca tat cct aaa gaa tca gag aaa atc atg ctt tca aag	1152	
Phe Leu His Pro Tyr Pro Lys Glu Ser Glu Lys Ile Met Leu Ser Lys		
370	375 380	
cag aca gga cta tcg aaa aac cag gtt gca aat tgg ttt att aac gcg	1200	
Gln Thr Gly Leu Ser Lys Asn Gln Val Ala Asn Trp Phe Ile Asn Ala		
385	390 395 400	
aga gtt cga cta tgg aaa cca atg att gaa gag atg tat aaa gaa gag	1248	
Arg Val Arg Leu Trp Lys Pro Met Ile Glu Glu Met Tyr Lys Glu Glu		
405	410 415	
ttt gga gaa tca gca gag tta ctc tct aac tct aat caa gac acc aaa	1296	
Phe Gly Glu Ser Ala Glu Leu Leu Ser Asn Ser Asn Gln Asp Thr Lys		
420	425 430	
aaa atg cag gaa aca tct cag ctc aaa cac gaa gac tct tcg tct tcg	1344	
Lys Met Gln Glu Thr Ser Gln Leu Lys His Glu Asp Ser Ser Ser Ser		
435	440 445	
caa caa cag aat cag gga aac aac aac aac aac atc cca tat aca tct	1392	
Gln Gln Gln Asn Gln Gly Asn Asn Asn Asn Asn Ile Pro Tyr Thr Ser		
450	455 460	
gat gca gaa caa aac cta gtc ttt gca gat cct aaa cca gac cgt gct	1440	
Asp Ala Glu Gln Asn Leu Val Phe Ala Asp Pro Lys Pro Asp Arg Ala		
465	470 475 480	
act act gga gat tac gac agc ttg atg aac tat cat ggg ttt ggt att	1488	
Thr Thr Gly Asp Tyr Asp Ser Leu Met Asn Tyr His Gly Phe Gly Ile		
485	490 495	
gat gat tac aat cgt tac gtt ggc ctt gga aac caa caa gat ggc aga	1536	
Asp Asp Tyr Asn Arg Tyr Val Gly Leu Gly Asn Gln Gln Asp Gly Arg		
500	505 510	
tat tct aat ccc cat caa tta cac gac ttt gtt gtc taa	1575	
Tyr Ser Asn Pro His Gln Leu His Asp Phe Val Val		
515	520	

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 <212> PRT
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<400> 46

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Ser Ser Ser Ala Ala Ser Phe Ser Glu Ile Val Ser Gly Asp Val Arg	
35 40 45	
Asn Asn Glu Met Val Phe Ile Pro Pro Thr Ser Asp Val Ala Val Asn	
50 55 60	
Gly Asn Val Thr Val Ser Ser Asn Asp Leu Ser Phe His Gly Gly Gly	
65 70 75 80	
Leu Ser Leu Ser Leu Gly Asn Gln Ile Gln Ser Ala Val Ser Val Ser	
85 90 95	

MBI15 Sequence Listing.ST25

Pro Phe Gln Tyr His Tyr Gln Asn Leu Ser Asn Gln Leu Ser Tyr Asn
 100 105 110
 Asn Leu Asn Pro Ser Thr Met Ser Asp Glu Asn Gly Lys Ser Leu Ser
 115 120 125
 Val His Gln His His Ser Asp Gln Ile Leu Pro Ser Ser Val Tyr Asn
 130 135 140
 Asn Asn Gly Asn Asn Gly Val Gly Phe Tyr Asn Asn Tyr Arg Tyr Glu
 145 150 155 160
 Thr Ser Gly Phe Val Ser Ser Val Leu Arg Ser Arg Tyr Leu Lys Pro
 165 170 175
 Thr Gln Gln Leu Leu Asp Glu Val Val Ser Val Arg Lys Asp Leu Lys
 180 185 190
 Leu Gly Asn Lys Lys Met Lys Asn Asp Lys Gly Gln Asp Phe His Asn
 195 200 205
 Gly Ser Ser Asp Asn Ile Thr Glu Asp Asp Lys Ser Gln Ser Gln Glu
 210 215 220
 Leu Ser Pro Ser Glu Arg Gln Glu Leu Gln Ser Lys Lys Ser Lys Leu
 225 230 235 240
 Leu Thr Met Val Asp Glu Val Asp Lys Arg Tyr Asn Gln Tyr His His
 245 250 255
 Gln Met Glu Ala Leu Ala Ser Ser Phe Glu Met Val Thr Gly Leu Gly
 260 265 270
 Ala Ala Lys Pro Tyr Thr Ser Val Ala Leu Asn Arg Ile Ser Arg His
 275 280 285
 Phe Arg Cys Leu Arg Asp Ala Ile Lys Glu Gln Ile Gln Val Ile Arg
 290 295 300
 Gly Lys Leu Gly Glu Arg Glu Thr Ser Asp Glu Gln Gly Glu Arg Ile
 305 310 315 320
 Pro Arg Leu Arg Tyr Leu Asp Gln Arg Leu Arg Gln Gln Arg Ala Leu
 325 330 335
 His Gln Gln Leu Gly Met Val Arg Pro Ala Trp Arg Pro Gln Arg Gly
 340 345 350
 Leu Pro Glu Asn Ser Val Ser Ile Leu Arg Ala Trp Leu Phe Glu His
 355 360 365
 Phe Leu His Pro Tyr Pro Lys Glu Ser Glu Lys Ile Met Leu Ser Lys
 370 375 380
 Gln Thr Gly Leu Ser Lys Asn Gln Val Ala Asn Trp Phe Ile Asn Ala
 385 390 395 400

MBI15 Sequence Listing.ST25

Arg Val Arg Leu Trp Lys Pro Met Ile Glu Glu Met Tyr Lys Glu Glu
405 410 415

Phe Gly Glu Ser Ala Glu Leu Leu Ser Asn Ser Asn Gln Asp Thr Lys
420 425 430

Lys Met Gln Glu Thr Ser Gln Leu Lys His Glu Asp Ser Ser Ser Ser
435 440 445

Gln Gln Gln Asn Gln Gly Asn Asn Asn Asn Asn Ile Pro Tyr Thr Ser
450 455 460

Asp Ala Glu Gln Asn Leu Val Phe Ala Asp Pro Lys Pro Asp Arg Ala
465 470 475 480

Thr Thr Gly Asp Tyr Asp Ser Leu Met Asn Tyr His Gly Phe Gly Ile
485 490 495

Asp Asp Tyr Asn Arg Tyr Val Gly Leu Gly Asn Gln Gln Asp Gly Arg
500 505 510

Tyr Ser Asn Pro His Gln Leu His Asp Phe Val Val
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<212> DNA
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<222> (73)..(1956)
<223> G965

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Met Gly Leu Ala Thr Thr Thr Ser Ser Met Ser Gln Asp
1 5 10
tat cat cat cac caa gga atc ttt tcc ttc tct aat gga ttc cac cga 159
Tyr His His His Gln Gly Ile Phe Ser Phe Ser Asn Gly Phe His Arg
15 20 25
tca tca tca acc act cat cag gag gaa gta gat gaa tcc gcc gtc gtc 207
Ser Ser Ser Thr Thr His Gln Glu Glu Val Asp Glu Ser Ala Val Val
30 35 40 45
tcc ggt gct caa att ccg gtt tat gaa acc gcc gga atg ttg tct gaa 255
Ser Gly Ala Gln Ile Pro Val Tyr Glu Thr Ala Gly Met Leu Ser Glu
50 55 60
atg ttt gct tac cct ggc gga ggt ggc ggc ggt tcc ggt gga gag att 303
Met Phe Ala Tyr Pro Gly Gly Gly Gly Gly Gly Ser Gly Gly Glu Ile
65 70 75
ctt gat cag tct act aaa cag ttg cta gag caa caa aac cgt cac aac 351
Leu Asp Gln Ser Thr Lys Gln Leu Leu Glu Gln Gln Asn Arg His Asn
80 85 90
aac aac aat aac tca act ctt cat atg tta tta cca aat cat cat caa 399
Asn Asn Asn Asn Ser Thr Leu His Met Leu Leu Pro Asn His His Gln
95 100 105

MBI15 Sequence Listing.ST25

ggt ttt gct ttc acc gac gaa aac act atg cag ccg cag caa caa caa Gly Phe Ala Phe Thr Asp Glu Asn Thr Met Gln Pro Gln Gln Gln Gln 110 115 120 125	447
cac ttt aca tgg cca tct tcc tcc tcc gat cat cat caa aac cga gat His Phe Thr Trp Pro Ser Ser Ser Ser Asp His His Gln Asn Arg Asp 130 135 140	495
atg atc gga acc gtc cac gtg gaa gga gga aag ggt ttg tct tta tct Met Ile Gly Thr Val His Val Glu Gly Gly Lys Gly Leu Ser Leu Ser 145 150 155	543
ctc tca tct tca tta gcc gca gct aaa gcc gag gaa tat aga agc att Leu Ser Ser Ser Leu Ala Ala Lys Ala Glu Glu Tyr Arg Ser Ile 160 165 170	591
tat tgt gca gcc gtt gat gga act tct tct tct tct aac gca tcc gct Tyr Cys Ala Ala Val Asp Gly Thr Ser Ser Ser Ser Asn Ala Ser Ala 175 180 185	639
cat cat cat caa ttc aat cag ttc aag aat ctt ctt ctt gag aat tct His His His Gln Phe Asn Gln Phe Lys Asn Leu Leu Leu Glu Asn Ser 190 195 200 205	687
tct tct caa cat cat cac cat caa gtt gtt gga cat ttt ggt tca tca Ser Ser Gln His His His His Gln Val Val Gly His Phe Gly Ser Ser 210 215 220	735
tca tca tct ccc atg gcg gct tct tca tcc att gga ggg atc tac acg Ser Ser Ser Pro Met Ala Ala Ser Ser Ser Ile Gly Gly Ile Tyr Thr 225 230 235	783
ttg agg aat tcg aaa tat acg aaa ccg gct caa gag ttg ttg gaa gag Leu Arg Asn Ser Lys Tyr Thr Lys Lys Pro Ala Gln Glu Leu Leu Glu Glu 240 245 250	831
ttt tgt agt gtt gga aga gga cat ttc aag aag aac aaa ctt agt agg Phe Cys Ser Val Gly Arg Gly His Phe Lys Lys Asn Lys Leu Ser Arg 255 260 265	879
aac aac tca aac cct aat act acc ggt gga gga gga ggc gga ggg tcc Asn Asn Ser Asn Pro Asn Thr Thr Gly Gly Gly Gly Gly Gly Ser 270 275 280 285	927
tcg tca tcg gcc gga aca gct aat gat agt cct cct ttg tct ccg gct Ser Ser Ser Ala Gly Thr Ala Asn Asp Ser Pro Pro Leu Ser Pro Ala 290 295 300	975
gat cgg att gaa cat caa aga aga aaa gtc aag cta cta tct atg ctt Asp Arg Ile Glu His Gln Arg Arg Lys Val Lys Leu Leu Ser Met Leu 305 310 315	1023
gaa gag gtg gac cga cgg tac aac cac tac tgc gaa caa atg caa atg Glu Glu Val Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln Met Gln Met 320 325 330	1071
gta gtg aac tca ttc gac caa gta atg ggt tac ggc gcg gcg gtt ccg Val Val Asn Ser Phe Asp Gln Val Met Gly Tyr Gly Ala Ala Val Pro 335 340 345	1119
tac acg aca tta gct caa aag gca atg tct agg cat ttc cgg tgt ttg Tyr Thr Thr Leu Ala Gln Lys Ala Met Ser Arg His Phe Arg Cys Leu 350 355 360 365	1167
aaa gac gcg gta gcg gtt cag ctt aaa cgc agc tgt gag ctt cta ggg Lys Asp Ala Val Ala Val Gln Leu Lys Arg Ser Cys Glu Leu Leu Gly 370 375 380	1215
gat aaa gag gcg gca ggg gct gca tcc tcg ggg tta acc aaa ggg gaa Asp Lys Glu Ala Ala Gly Ala Ala Ser Ser Gly Leu Thr Lys Gly Glu 385 390 395	1263
acg ccg cga ttg cgt ttg cta gag cag agt ttg cgt cag caa cga gcg Thr Pro Arg Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln Gln Arg Ala 1311	1311

MBI15 Sequence Listing.ST25

400	405	410	
ttt cat cat atg ggt atg atg gag caa gag gca tgg aga ccg caa cgt Phe His His Met Gly Met Met Glu Gln Glu Ala Trp Arg Pro Gln Arg 415 420 425			1359
ggt ttg cct gaa cgc tcc gtt aat atc ctt aga gct tgg cta ttc gag Gly Leu Pro Glu Arg Ser Val Asn Ile Leu Arg Ala Trp Leu Phe Glu 430 435 440 445			1407
cat ttt ctt aat ccg tac cca agc gat gct gat aag cac ctc tta gca His Phe Leu Asn Pro Tyr Pro Ser Asp Ala Asp Lys His Leu Leu Ala 450 455 460			1455
cga cag act ggt tta tcc aga aat cag gtg tca aat tgg ttc ata aat Arg Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile Asn 465 470 475			1503
gct agg gtt cgc cta tgg aaa cca atg gtg gaa gag atg tat caa caa Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr Gln Gln 480 485 490			1551
gaa gca aaa gaa aga gaa gaa gca gaa gaa gaa aat gaa aat caa caa Glu Ala Lys Glu Arg Glu Glu Ala Glu Glu Glu Asn Glu Asn Gln Gln 495 500 505			1599
caa caa aga aga cag caa caa aca aac aac aac gac acg aaa ccc aac Gln Gln Arg Arg Gln Gln Gln Thr Asn Asn Asn Asp Thr Lys Pro Asn 510 515 520 525			1647
aac aat gaa aac aac ttc act gtc ata acc gca caa act cca acg acg Asn Asn Glu Asn Asn Phe Thr Val Ile Thr Ala Gln Thr Pro Thr Thr 530 535 540			1695
atg aca tcg aca cat cac gaa aac gac tct tca ttc ctc tct tcc gtc Met Thr Ser Thr His His Glu Asn Asp Ser Ser Phe Leu Ser Ser Val 545 550 555			1743
gcc gcc gct tct cac ggc ggt tca gac gcg ttc acc gtc gcc acg tgt Ala Ala Ala Ser His Gly Gly Ser Asp Ala Phe Thr Val Ala Thr Cys 560 565 570			1791
cag caa gac gtc agt gac ttc cac gtc gac gga gat ggt gtg aac gtc Gln Gln Asp Val Ser Asp Phe His Val Asp Gly Asp Gly Val Asn Val 575 580 585			1839
ata aga ttc ggg acc aaa cag act ggt gac gtg tct ctt acg ctt ggt Ile Arg Phe Gly Thr Lys Gln Thr Gly Asp Val Ser Leu Thr Leu Gly 590 595 600 605			1887
cta cgc cac tct ggc aat att cct gat aag aac act tct ttc tcc gtt Leu Arg His Ser Gly Asn Ile Pro Asp Lys Asn Thr Ser Phe Ser Val 610 615 620			1935
aga gac ttt gga gat ttt tag tcttctttgt ttctcaattt attcatc Arg Asp Phe Gly Asp Phe 625			1983

<210> 48
 <211> 627
 <212> PRT
 <213> Arabidopsis thaliana

<400> 48

Met Gly Leu Ala Thr Thr Thr Ser Ser Met Ser Gln Asp Tyr His His
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His Gln Gly Ile Phe Ser Phe Ser Asn Gly Phe His Arg Ser Ser Ser
 20 25 30

Thr Thr His Gln Glu Glu Val Asp Glu Ser Ala Val Val Ser Gly Ala

MBI15 Sequence Listing.ST25
40 45

35

Gln Ile Pro Val Tyr Glu Thr Ala Gly Met Leu Ser Glu Met Phe Ala
50 55 60

Tyr Pro Gly Gly Gly Gly Gly Gly Ser Gly Gly Glu Ile Leu Asp Gln
65 70 75 80

Ser Thr Lys Gln Leu Leu Glu Gln Gln Asn Arg His Asn Asn Asn Asn
85 90 95

Asn Ser Thr Leu His Met Leu Leu Pro Asn His His Gln Gly Phe Ala
100 105 110

Phe Thr Asp Glu Asn Thr Met Gln Pro Gln Gln Gln Gln His Phe Thr
115 120 125

Trp Pro Ser Ser Ser Ser Asp His His Gln Asn Arg Asp Met Ile Gly
130 135 140

Thr Val His Val Glu Gly Gly Lys Gly Leu Ser Leu Ser Leu Ser Ser
145 150 155 160

Ser Leu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Ser Ile Tyr Cys Ala
165 170 175

Ala Val Asp Gly Thr Ser Ser Ser Ser Asn Ala Ser Ala His His His
180 185 190

Gln Phe Asn Gln Phe Lys Asn Leu Leu Leu Glu Asn Ser Ser Ser Gln
195 200 205

His His His His Gln Val Val Gly His Phe Gly Ser Ser Ser Ser Ser
210 215 220

Pro Met Ala Ala Ser Ser Ser Ile Gly Gly Ile Tyr Thr Leu Arg Asn
225 230 235 240

Ser Lys Tyr Thr Lys Pro Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser
245 250 255

Val Gly Arg Gly His Phe Lys Lys Asn Lys Leu Ser Arg Asn Asn Ser
260 265 270

Asn Pro Asn Thr Thr Gly Gly Gly Gly Gly Gly Gly Ser Ser Ser Ser
275 280 285

Ala Gly Thr Ala Asn Asp Ser Pro Pro Leu Ser Pro Ala Asp Arg Ile
290 295 300

Glu His Gln Arg Arg Lys Val Lys Leu Leu Ser Met Leu Glu Glu Val
305 310 315 320

Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln Met Gln Met Val Val Asn
325 330 335

MBI15 Sequence Listing.ST25

Ser Phe Asp Gln Val Met Gly Tyr Gly Ala Ala Val Pro Tyr Thr Thr
 340 345 350
 Leu Ala Gln Lys Ala Met Ser Arg His Phe Arg Cys Leu Lys Asp Ala
 355 360 365
 Val Ala Val Gln Leu Lys Arg Ser Cys Glu Leu Leu Gly Asp Lys Glu
 370 375 380
 Ala Ala Gly Ala Ala Ser Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg
 385 390 395 400
 Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln Gln Arg Ala Phe His His
 405 410 415
 Met Gly Met Met Glu Gln Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro
 420 425 430
 Glu Arg Ser Val Asn Ile Leu Arg Ala Trp Leu Phe Glu His Phe Leu
 435 440 445
 Asn Pro Tyr Pro Ser Asp Ala Asp Lys His Leu Leu Ala Arg Gln Thr
 450 455 460
 Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val
 465 470 475 480
 Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr Gln Gln Glu Ala Lys
 485 490 495
 Glu Arg Glu Glu Ala Glu Glu Glu Asn Glu Asn Gln Gln Gln Gln Arg
 500 505 510
 Arg Gln Gln Gln Thr Asn Asn Asn Asp Thr Lys Pro Asn Asn Asn Glu
 515 520 525
 Asn Asn Phe Thr Val Ile Thr Ala Gln Thr Pro Thr Thr Met Thr Ser
 530 535 540
 Thr His His Glu Asn Asp Ser Ser Phe Leu Ser Ser Val Ala Ala Ala
 545 550 555 560
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 565 570 575
 Val Ser Asp Phe His Val Asp Gly Asp Gly Val Asn Val Ile Arg Phe
 580 585 590
 Gly Thr Lys Gln Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His
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MBI15 Sequence Listing.ST25

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aag ctg atg gaa gaa aac gtt gga gca gcg atg caa ctt ttg caa tca				938
Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser	255	260	265	
aag gct ctt tgc ata atg ccg atc tca ttg gca atg gcg att tac cat				986
Lys Ala Leu Cys Ile Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His	270	275	280	
tct cag cca cca gac aca tct tct tca atc gtc aaa cca gag atg aat				1034
Ser Gln Pro Pro Asp Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn	285	290	295	
cct cca ccg tag atttttgttc atccaacggg cccagctga tgattgacat				1086
Pro Pro Pro	300			
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ggagatggaa tctaagtagg atttgtgcag taaagaagta aaacgggatc tgtcaaaaga				1206
aggaaaaagc tctcgcttgc ttggctagta tttatcattt tgatgaaagt aactcttttt				1266
tgttcaaaga ctttagtggtg attttcagga ccaagggctt tgagggtagt gctagctgta				1326
gtaatagtaa tgaagggtgtg ggatcgtgtt tttgaattat gtaaaaaagg aagaaaaaac				1386
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<400> 50

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Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly Gly Val Gly Pro Pro
 35 40 45

Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu Gly Asn His Asn His
 50 55 60

Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly Phe His Asn Gln Met
 65 70 75 80

Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly His Gly Phe Leu
 85 90 95

Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp Asp Val Leu Asp Asn
 100 105 110

Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly Gln Pro Met Ser Gln
 115 120 125

Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr Ile Arg Pro Arg Val

MBI15 Sequence Listing.ST25

130 135 140

Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala Glu Arg
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Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ser Leu Gln Glu Leu
165 170 175

Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp Glu Ile
180 185 190

Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu Ser Met
195 200 205

Ser Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr Glu Met
210 215 220

Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gln Ala Val Trp Glu Lys
225 230 235 240

Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu
245 250 255

Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Ile
260 265 270

Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp
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Met Asp Tyr Lys Val Ser
1 5
aga agt ggg gag ata gta gaa gga gaa gta gaa gat tca gaa aag att 161
Arg Ser Gly Glu Ile Val Glu Gly Glu Val Glu Asp Ser Glu Lys Ile
10 15 20
gat tta cca cct ggt ttc aga ttt cac cca act gat gaa gaa ctt ata 209
Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile
25 30 35
aca cac tat cta aga cca aag gtt gta aac tct ttt ttc tct gct ata 257
Thr His Tyr Leu Arg Pro Lys Val Val Asn Ser Phe Phe Ser Ala Ile
40 45 50
gct att ggt gaa gtt gat ctc aac aaa gtc gag cct tgg gac ttg cct 305
Ala Ile Gly Glu Val Asp Leu Asn Lys Val Glu Pro Trp Asp Leu Pro

MBI15 Sequence Listing.ST25

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Asp Arg Lys Tyr Pro	Thr Gly Leu Arg Thr	Asn Arg Ala Thr Lys Ala		
	90	95	100	
ggt tat tgg aaa gct aca	ggg aaa gat aaa gag atc	ttc aaa ggg aaa		449
Gly Tyr Trp Lys Ala	Thr Gly Lys Asp Lys	Glu Ile Phe Lys Gly Lys		
	105	110	115	
tct ctt gtt ggt atg aag	aaa aca ttg gtt ttc	tac aaa gga aga gct		497
Ser Leu Val Gly Met	Lys Lys Thr Leu Val	Phe Tyr Lys Gly Arg Ala		
	120	125	130	
cct aaa gga gta aaa aca	aat tgg gtc atg cat	gag tat cga tta gaa		545
Pro Lys Gly Val Lys	Thr Asn Trp Val Met	His Glu Tyr Arg Leu Glu		
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ggc aaa ttc gct atc gat	aat ctc tct aaa acc	gct aag aac gaa tgt		593
Gly Lys Phe Ala Ile	Asp Asn Leu Ser Lys	Thr Ala Lys Asn Glu Cys		
	155	160	165	
gtt att agt cgt gtt ttt	cat aca cgg act gat	ggt acg aag gag cat		641
Val Ile Ser Arg Val	Phe His Thr Arg Thr	Asp Gly Thr Lys Glu His		
	170	175	180	
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Met Ser Val Gly Leu	Pro Pro Leu Met Asp	Ser Ser Pro Tyr Leu Lys		
	185	190	195	
agt aga gga caa gac tct	tta gcc ggg acc acc	ctt ggt ggg ttg ttg		737
Ser Arg Gly Gln Asp	Ser Leu Ala Gly Thr	Thr Leu Gly Gly Leu Leu		
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tct cac gtt acc tac ttc	tcc gac caa aca acc	gat gac aag agt ctt		785
Ser His Val Thr Tyr	Phe Ser Asp Gln Thr	Thr Asp Asp Lys Ser Leu		
	215	220	225	230
gtg gcc gat ttt aaa act	acc atg ttt ggt tcc	gga tgc act aac ttt		833
Val Ala Asp Phe Lys	Thr Thr Met Phe Gly	Ser Gly Ser Thr Asn Phe		
	235	240	245	
tta cca aac ata ggt tct	cta cta gac ttc gat	cct ctg ttt cta caa		881
Leu Pro Asn Ile Gly	Ser Leu Leu Asp Phe	Asp Pro Leu Phe Leu Gln		
	250	255	260	
aac aat tct tca gta ctg	aag atg ttg ctt gac	aat gaa gaa acc caa		929
Asn Asn Ser Ser Val	Leu Lys Met Leu Leu	Asp Asn Glu Glu Thr Gln		
	265	270	275	
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Phe Lys Lys Asn Leu	His Asn Ser Gly Ser	Ser Glu Ser Glu Leu Thr		
	280	285	290	
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	315			
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MBI15 Sequence Listing.ST25

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 35 40 45

Ser Phe Phe Ser Ala Ile Ala Ile Gly Glu Val Asp Leu Asn Lys Val
 50 55 60

Glu Pro Trp Asp Leu Pro Trp Lys Ala Lys Leu Gly Glu Lys Glu Trp
 65 70 75 80

Tyr Phe Phe Cys Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr
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Asn Arg Ala Thr Lys Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys
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Glu Ile Phe Lys Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val
 115 120 125

Phe Tyr Lys Gly Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met
 130 135 140

His Glu Tyr Arg Leu Glu Gly Lys Phe Ala Ile Asp Asn Leu Ser Lys
 145 150 155 160

Thr Ala Lys Asn Glu Cys Val Ile Ser Arg Val Phe His Thr Arg Thr
 165 170 175

Asp Gly Thr Lys Glu His Met Ser Val Gly Leu Pro Pro Leu Met Asp
 180 185 190

Ser Ser Pro Tyr Leu Lys Ser Arg Gly Gln Asp Ser Leu Ala Gly Thr
 195 200 205

Thr Leu Gly Gly Leu Leu Ser His Val Thr Tyr Phe Ser Asp Gln Thr
 210 215 220

Thr Asp Asp Lys Ser Leu Val Ala Asp Phe Lys Thr Thr Met Phe Gly
 225 230 235 240

Ser Gly Ser Thr Asn Phe Leu Pro Asn Ile Gly Ser Leu Leu Asp Phe
 245 250 255

Asp Pro Leu Phe Leu Gln Asn Asn Ser Ser Val Leu Lys Met Leu Leu
 260 265 270

Asp Asn Glu Glu Thr Gln Phe Lys Lys Asn Leu His Asn Ser Gly Ser
 275 280 285

MBI15 Sequence Listing.ST25

Ser Glu Ser Glu Leu Thr Ala Ser Ser Trp Gln Gly His Asn Ser Tyr
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 Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro Thr Leu Phe Gln
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 Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys Arg Ser Lys Arg
 25 30 35
 tca aga tct gaa ttc gac cgt cag agt ctc acg gag gat gaa tat atc 198
 Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu Asp Glu Tyr Ile
 40 45 50
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 Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp Arg Asn Arg Asp
 55 60 65
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 Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu Leu Pro Pro Leu
 70 75 80
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 Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys Ala Phe Ser Ser
 85 90 95 100
 tac cag gct ctt ggt gga cac aag gca agt cac cgg aaa agc ttt tcg 390
 Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ser Phe Ser
 105 110 115
 ctt act caa tct gcc gga gga gat gag ctg tcg aca tcg tcg gcg ata 438
 Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr Ser Ser Ala Ile
 120 125 130
 acc acg tct ggt ata tcc ggt ggc ggg gga gga agt gtg aag tcg cac 486
 Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser Val Lys Ser His
 135 140 145
 gtt tgc tct atc tgt cat aaa tcg ttc gcc acc ggt caa gct ctc ggc 534
 Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly Gln Ala Leu Gly
 150 155 160
 ggc cac aaa cgg tgc cac tac gaa gga aag aac gga ggc ggt gtg agt 582
 Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly Gly Gly Val Ser
 165 170 175 180
 agt agc gtg tcg aat tct gaa gat gtg ggg tct aca agc cac gtc agc 630
 Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr Ser His Val Ser
 185 190 195
 agt ggc cac cgt ggg ttt gac ctc aac ata ccg ccg ata ccg gaa ttc 678

MBI15 Sequence Listing.ST25

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 200 205 210

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 215 220 225

aaa ctc cgg ttt gac ttc ccg gag aaa ccc taa acataaacct aggaaaaact 779
 Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
 230 235

ttacagaatt cattttatag gaaattgttt tactgtatat acaaatatcg attttgattg 839
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Arg Ser Lys Arg Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu
 35 40 45

Asp Glu Tyr Ile Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp
 50 55 60

Arg Asn Arg Asp Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu
 65 70 75 80

Leu Pro Pro Leu Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys
 85 90 95

Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
 100 105 110

Lys Ser Phe Ser Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr
 115 120 125

Ser Ser Ala Ile Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Ser
 130 135 140

Val Lys Ser His Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly
 145 150 155 160

Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly
 165 170 175

Gly Gly Val Ser Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr
 180 185 190

Ser His Val Ser Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro
 195 200 205

MBI15 Sequence Listing.ST25

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Pro Phe Asp Leu His Phe Ser Gly Lys Leu Pro Lys Arg Glu Val Ser
10 15 20

gct tca gct tct aaa gtt gta gag aag aaa tgg tta gtg aaa gat gag 150
Ala Ser Ala Ser Lys Val Val Glu Lys Lys Trp Leu Val Lys Asp Glu
25 30 35 40

aag aga aat atg cta caa gat gaa ata aac cgg gtt aat tcg gag aac 198
Lys Arg Asn Met Leu Gln Asp Glu Ile Asn Arg Val Asn Ser Glu Asn
45 50 55

aag aag cta acc gaa atg tta gca aga gtc tgt gag aag tac tat gct 246
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Lys Tyr Tyr Ala
60 65 70

ctt aat aat ctt atg gag gag ttg cag agt cga aag agt cct gaa agt 294
Leu Asn Asn Leu Met Glu Glu Leu Gln Ser Arg Lys Ser Pro Glu Ser
75 80 85

gtt aac ttt cag aac aaa cag cta acg ggg aaa cga aaa caa gaa ctt 342
Val Asn Phe Gln Asn Lys Gln Leu Thr Gly Lys Arg Lys Gln Glu Leu
90 95 100

gat gag ttt gtt agc tcc cca att gga ctc agt ctc gga cca atc gag 390
Asp Glu Phe Val Ser Ser Pro Ile Gly Leu Ser Leu Gly Pro Ile Glu
105 110 115 120

aac atc acc aac gat aaa gcg acg gtt tca acc gct tac ttt gct gct 438
Asn Ile Thr Asn Asp Lys Ala Thr Val Ser Thr Ala Tyr Phe Ala Ala
125 130 135

gag aag tct gac aca agc ttg act gtg aaa gat gga tat caa tgg agg 486
Glu Lys Ser Asp Thr Ser Leu Thr Val Lys Asp Gly Tyr Gln Trp Arg
140 145 150

aaa tac ggg caa aag att acg aga gat aat cca tct cct aga gct tac 534
Lys Tyr Gly Gln Lys Ile Thr Arg Asp Asn Pro Ser Pro Arg Ala Tyr
155 160 165

ttc aga tgc tcg ttt tca ccg tct tgt cta gtc aag aag aag gtg caa 582
Phe Arg Cys Ser Phe Ser Pro Ser Cys Leu Val Lys Lys Lys Val Gln
170 175 180

cga agt gca gaa gat cca tct ttc ttg gta gcc act tac gaa ggg aca 630
Arg Ser Ala Glu Asp Pro Ser Phe Leu Val Ala Thr Tyr Glu Gly Thr
185 190 195 200

cat aac cac acc gga cca cat gca agt gtg tcc agg aca gtg aaa ctt 678

MBI15 Sequence Listing.ST25

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 220 225 230

ggg acg att caa gag gtt ttg gtg caa caa atg gct tct tcg ttg acc 774
 Gly Thr Ile Gln Glu Val Leu Val Gln Gln Met Ala Ser Ser Leu Thr
 235 240 245

aaa gat cct aag ttc act gca gct ctt gcg act gct att tcc ggg aga 822
 Lys Asp Pro Lys Phe Thr Ala Ala Leu Ala Thr Ala Ile Ser Gly Arg
 250 255 260

ttg ata gag cat tca aga aca tga aagttctcta gaacatgtat atttctgttt 876
 Leu Ile Glu His Ser Arg Thr
 265 270

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aagggtcacc cccattttat cttatg 1022

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Lys Lys Trp Leu Val Lys Asp Glu Lys Arg Asn Met Leu Gln Asp Glu
 35 40 45

Ile Asn Arg Val Asn Ser Glu Asn Lys Lys Leu Thr Glu Met Leu Ala
 50 55 60

Arg Val Cys Glu Lys Tyr Tyr Ala Leu Asn Asn Leu Met Glu Glu Leu
 65 70 75 80

Gln Ser Arg Lys Ser Pro Glu Ser Val Asn Phe Gln Asn Lys Gln Leu
 85 90 95

Thr Gly Lys Arg Lys Gln Glu Leu Asp Glu Phe Val Ser Ser Pro Ile
 100 105 110

Gly Leu Ser Leu Gly Pro Ile Glu Asn Ile Thr Asn Asp Lys Ala Thr
 115 120 125

Val Ser Thr Ala Tyr Phe Ala Ala Glu Lys Ser Asp Thr Ser Leu Thr
 130 135 140

Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Ile Thr Arg
 145 150 155 160

Asp Asn Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ser Pro Ser
 165 170 175

MBI15 Sequence Listing.ST25

Cys Leu Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro Ser Phe
180 185 190

Leu Val Ala Thr Tyr Glu Gly Thr His Asn His Thr Gly Pro His Ala
195 200 205

Ser Val Ser Arg Thr Val Lys Leu Asp Leu Val Gln Gly Gly Leu Glu
210 215 220

Pro Val Glu Glu Lys Lys Glu Arg Gly Thr Ile Gln Glu Val Leu Val
225 230 235 240

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245 250 255

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260 265 270

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<223> G1349

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gtt caa cca gac gcc cgt acc gtc caa tgc tca acc tgc cac acc gtc 96
Val Gln Pro Asp Ala Arg Thr Val Gln Cys Ser Thr Cys His Thr Val
20 25 30
acg cag ctc tac tcg cta gtg gac ata gct cgc ggt gca aac cgc ata 144
Thr Gln Leu Tyr Ser Leu Val Asp Ile Ala Arg Gly Ala Asn Arg Ile
35 40 45
att cat ggg ttt caa cag cta ctt aga caa cac caa ccg caa cat cat 192
Ile His Gly Phe Gln Gln Leu Leu Arg Gln His Gln Pro Gln His His
50 55 60
gaa caa caa caa caa caa atg atg gct caa ccg cca cca cgg ctg ctt 240
Glu Gln Gln Gln Gln Gln Met Met Ala Gln Pro Pro Pro Arg Leu Leu
65 70 75 80
gag cct ctt ccc tcg ccg ttt ggg aag aag aga gca gtt tta tgc ggc 288
Glu Pro Leu Pro Ser Pro Phe Gly Lys Lys Arg Ala Val Leu Cys Gly
85 90 95
gtg aac tat aag gga aaa agt tat agc ttg aaa ggt tgc atc agt gat 336
Val Asn Tyr Lys Gly Lys Ser Tyr Ser Leu Lys Gly Cys Ile Ser Asp
100 105 110
gct aag tcc atg aga tct tta ttg gtt caa caa atg ggt ttc cct att 384
Ala Lys Ser Met Arg Ser Leu Leu Val Gln Gln Met Gly Phe Pro Ile
115 120 125
gac tct att ctc atg ctc aca gaa gat gaa gcc agc ccg cag aga ata 432
Asp Ser Ile Leu Met Leu Thr Glu Asp Glu Ala Ser Pro Gln Arg Ile
130 135 140
ccg acg aag aga aac att agg aag gcg atg aga tgg tta gtt gaa ggg 480

MBI15 Sequence Listing.ST25

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Pro Thr Lys Arg Asn Ile Arg Lys Ala Met Arg Trp Leu Val Glu Gly
145      150      155      160
aac aga gca agg gac tca cta gtg ttc cat ttc tct ggt cat gga tct      528
Asn Arg Ala Arg Asp Ser Leu Val Phe His Phe Ser Gly His Gly Ser
165      170      175
cag cag aat gac tac aac gga gac gag atc gat ggt caa gat gaa gcc      576
Gln Gln Asn Asp Tyr Asn Gly Asp Glu Ile Asp Gly Gln Asp Glu Ala
180      185      190
ttg tgc cct tta gac cat gaa aca gaa gga aaa atc att gat gac gag      624
Leu Cys Pro Leu Asp His Glu Thr Glu Gly Lys Ile Ile Asp Asp Glu
195      200      205
att aac cgg ata ctc gtg agg cct ctc gtc cat gga gct aag ctt cac      672
Ile Asn Arg Ile Leu Val Arg Pro Leu Val His Gly Ala Lys Leu His
210      215      220
gct gtc atc gac gcc tgt aac agc ggg act gtc ctt gat tta ccc ttc      720
Ala Val Ile Asp Ala Cys Asn Ser Gly Thr Val Leu Asp Leu Pro Phe
225      230      235
att tgc agg atg gag agg aat ggt tct tat gaa tgg gaa gac cat aga      768
Ile Cys Arg Met Glu Arg Asn Gly Ser Tyr Glu Trp Glu Asp His Arg
245      250      255
tca gtc aga gct tac aaa gga aca gat ggt gga gca gct ttc tgt ttc      816
Ser Val Arg Ala Tyr Lys Gly Thr Asp Gly Gly Ala Ala Phe Cys Phe
260      265      270
agt gct tgt gac gat gat gaa tcc agt ggt tac act cct gtg ttc acg      864
Ser Ala Cys Asp Asp Asp Glu Ser Ser Gly Tyr Thr Pro Val Phe Thr
275      280      285
ggg aag aac aca gga gcc atg act tat agc ttc ata aag gcg gtg aag      912
Gly Lys Asn Thr Gly Ala Met Thr Tyr Ser Phe Ile Lys Ala Val Lys
290      295      300
aca gct gga cca gca ccc acg tat ggc cac ctg ctt aac ctt atg tgt      960
Thr Ala Gly Pro Ala Pro Thr Tyr Gly His Leu Leu Asn Leu Met Cys
305      310      315
tct gca ata cga gag gcc cag tct cgc ctc gcc ttt aac ggg gac tac      1008
Ser Ala Ile Arg Glu Ala Gln Ser Arg Leu Ala Phe Asn Gly Asp Tyr
325      330      335
aca agc tct gat gca tcc gcg gag cca ctg cta aca tca tct gag gaa      1056
Thr Ser Ser Asp Ala Ser Ala Glu Pro Leu Leu Thr Ser Ser Glu Glu
340      345      350
ttt gac gtg tac gcg aca aag ttt gta ctc tga atgctgtaca tatgatgctg      1109
Phe Asp Val Tyr Ala Thr Lys Phe Val Leu
355      360
caaatagctc ggaaacgttt ctatgtgtat gtatcatgta atgattatgt tgcatagcct      1169
ctctcttctt acgagcaata agctatgaaa taattgattc gctaagaaat ttaaaatgaa      1229
a                                                                 1230

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<210> 58
 <211> 362
 <212> PRT
 <213> Arabidopsis thaliana

<400> 58

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Met Ala Ser Arg Arg Glu Val Arg Cys Arg Cys Gly Arg Arg Met Trp
1      5      10      15

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Val Gln Pro Asp Ala Arg Thr Val Gln Cys Ser Thr Cys His Thr Val
20      25      30

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MBI15 Sequence Listing.ST25

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Thr Gln Leu Tyr Ser Leu Val Asp Ile Ala Arg Gly Ala Asn Arg Ile
    35          40          45

Ile His Gly Phe Gln Gln Leu Leu Arg Gln His Gln Pro Gln His His
    50          55          60

Glu Gln Gln Gln Gln Gln Met Met Ala Gln Pro Pro Pro Arg Leu Leu
    65          70          75          80

Glu Pro Leu Pro Ser Pro Phe Gly Lys Lys Arg Ala Val Leu Cys Gly
    85          90          95

Val Asn Tyr Lys Gly Lys Ser Tyr Ser Leu Lys Gly Cys Ile Ser Asp
    100         105         110

Ala Lys Ser Met Arg Ser Leu Leu Val Gln Gln Met Gly Phe Pro Ile
    115         120         125

Asp Ser Ile Leu Met Leu Thr Glu Asp Glu Ala Ser Pro Gln Arg Ile
    130         135         140

Pro Thr Lys Arg Asn Ile Arg Lys Ala Met Arg Trp Leu Val Glu Gly
    145         150         155         160

Asn Arg Ala Arg Asp Ser Leu Val Phe His Phe Ser Gly His Gly Ser
    165         170         175

Gln Gln Asn Asp Tyr Asn Gly Asp Glu Ile Asp Gly Gln Asp Glu Ala
    180         185         190

Leu Cys Pro Leu Asp His Glu Thr Glu Gly Lys Ile Ile Asp Asp Glu
    195         200         205

Ile Asn Arg Ile Leu Val Arg Pro Leu Val His Gly Ala Lys Leu His
    210         215         220

Ala Val Ile Asp Ala Cys Asn Ser Gly Thr Val Leu Asp Leu Pro Phe
    225         230         235         240

Ile Cys Arg Met Glu Arg Asn Gly Ser Tyr Glu Trp Glu Asp His Arg
    245         250         255

Ser Val Arg Ala Tyr Lys Gly Thr Asp Gly Gly Ala Ala Phe Cys Phe
    260         265         270

Ser Ala Cys Asp Asp Asp Glu Ser Ser Gly Tyr Thr Pro Val Phe Thr
    275         280         285

Gly Lys Asn Thr Gly Ala Met Thr Tyr Ser Phe Ile Lys Ala Val Lys
    290         295         300

Thr Ala Gly Pro Ala Pro Thr Tyr Gly His Leu Leu Asn Leu Met Cys
    305         310         315         320

Ser Ala Ile Arg Glu Ala Gln Ser Arg Leu Ala Phe Asn Gly Asp Tyr

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MBI15 Sequence Listing.ST25
330

325

335

Thr Ser Ser Asp Ala Ser Ala Glu Pro Leu Leu Thr Ser Ser Glu Glu
340 345 350

Phe Asp Val Tyr Ala Thr Lys Phe Val Leu
355 360

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A01H 1/00, 5/00; C12N 5/14, 15/82

US CL : 435/320.1, 419, 468; 800/278, 279, 287, 301, 305-310, 312, 314, 317, 320, 322

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 419, 468; 800/278, 279, 287, 301, 305-310, 312, 314, 317, 320, 322

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EAST, USPAT; STN, Agricola, CaPlus, Biosis, Embase**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 97/47183 A1 (PURDUE RESEARCH FOUNDATION) 18 December 1997 (18.12.1997), entire reference.	1-9, 12, 13, 25 ----- 10, 11, 26, 27
X --- Y	US 5,939,601 (KLESSIG et al) 17 August 1999 (17.08.1999), entire reference.	1-9, 12, 13, 25 ----- 10, 11, 26, 27
A	Database Genbank on NCBI, US National Library of Medicine, (Bethesda, MD, USA) No. AB009055, SATO, S. et al 'Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned P1 and TAC clones. 27 December 2000, DNA RES. 1998, Vol. 5, No. 1, pages 41-54, see bases 16,003-16,490, 16,571-16,683 and 16,780-17,365.	1-13, 25-27



Further documents are listed in the continuation of Box C.



See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

23 February 2001 (23.02.2001)

Date of mailing of the international search report

09 MAR 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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TERRY J. DEY

PARALEGAL SPECIALIST

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claim Nos.: 14
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-13 & 25-27 and SEQ ID NOs 1&2

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I-XXIX, claim(s) 1-14 and 25-27, drawn to a transgenic plant having modified seed characteristics, polynucleotides and vectors for producing said transgenic plant and a method of making said transgenic plant. Applicant must elect one pair of sequences (one nucleic acid and the corresponding amino acid translation) to be examined, *i.e.* SEQ ID NO: 1 and 2 in Group I, SEQ ID NO: 3 and 4 in Group II, SEQ ID NO: 5 and 6 in Group III, etc.

Group XXX, claim(s) 15-17, drawn to a method of identifying a factor that is modulated.

Group XXXI, claims(s) 18, drawn to a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide.

Group XXXII, claims(s) 19 and 20, drawn to an integrated computer system.

Group XXXIII, claim(s) 21-24, drawn to a method for identifying a polynucleotide sequence comprising selecting a nucleic acid sequence from a database that meets a selected sequence criteria.

The inventions listed as Groups I-XXXIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-XXXIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I-XXIX are drawn to a transgenic plant and a method of producing said plant with a nucleic acid sequence. The methods of Groups I-XXIX differ from each other in that they are directed to a plant transformation method and transgenic plant with a structurally and functionally distinct nucleic acid sequence which encodes a structurally and functionally distinct amino acid sequence. In addition, Groups XXX, XXXI and XXXII are different methods from any of Groups I-XXIX in that they have different method steps and different end products, and Group XXXII requires a computer system. Thus, there is no single special technical feature, which links the inventions of Groups I-XXXIII under PCT Rule 13.2.

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